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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 17, 2003, 22:38:40; Search time 12 Seconds (without alignments) 1779.177 Million cell updates/sec Run on:

US-10-098-602A-2 2376 1 MTITYDELNNLIRNGKIDTV......INEFSKQVTDWELNQGFNRY 454 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

P15106 streptomyce P28605 synechococc	Q59747 rhizobium m P43794 haemophilus	P15124 methylococc Q9clp2 pasteurella	P10583 azospirillu P19904 vibrio algi	P22248 azotobacter P94126 azorhizobiu	P94845 helicobacte	P28786 proteus vul
GLNA_STRCO GLNA_SYNP2	GLN1_RHIME GLNA_HAEIN	GLNA_METCA GLNA_PASMU	GLNA_AZOBR GLNA_VIBAL	GLNA_AZOVI GLNA_AZOCA	GLNA_HELPY	GLNA_PROVU
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469	469	468	468 468	467	481	469
12.6	12.1	11.9	11.8	11.6	11.3	11.3
299	287.5	283 283	280 278.5	276	269	267.5
3.34 5.4	36	38 38	40	4 4 3 6	44	45

ALIGNMENTS

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237
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                                                                                                                                                                                                                                                                                                                                                                                                                LPLŚKVEBIRRDIAIALEKWGITVEATHHĘVAPŚCHĘVDFRYDTFLKTADNAQTVKLVIK 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 ILKHAKALAAVTNPTINSYKRLVPGYBAPVYISWSVGNRSALIRIPKARGKATRLEYRSP 333 324 524 538 344 554 559 353 355 GADLNPYLAFSAIIAAGISGIEEKLELPPPASGNVYN-----DKELPEFPNSLQNATH 407
                                                                                                                                                                                                                                                                                           dimepdesgiegevrieesomylkpvldpreavlpwtvdgaksarvicdvytp----DGKPF 101
                                                                                                                                                                                                                                                                                                                          50 2 25 FCSPRVILMQQIERLANLKIKGLFASELEFNLFNETYKSASQKHWKNLKTAQPHHQWMNI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLKYVPEATYFFASYINSYKRLOPLTFAPTKCCWAIDNRTSAFRLCNSKSEGINVELRIG 354
                                                                                                                                                                                                                                                                                      GIAGGGYEISS-VDTGYSDCHLCADLNSLHLLPWS-EGA----VLAISNPHNFVTSEPL 114
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                                                                                                                                                                                                                                                  TWAIFHGYHATEMPKPFYGWISGMHYHMSL--FRGDRNAFYDPDDPLGLSKELRYFVGG
                                                                                                                                                                                                                                  3 ITYDELNNLIRNGKIDTVVLACVDMQGRLMGKRLTGRHFLGLDQKKISISTFVYAVTIB-
                                                                                                                                                                                                           42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=P262;
MEDLINE=88086901; PubMed=2891680;
Janssen P.J., Jones W.A., Jones D.T., Woods D.R.;
"Molecular analysis regulation of the glnA gene of the Gram-molecular analysis regulation acetobutylicum.";
J. Bacteriol. 170:400-408(1988).
-! CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium saccharobutylicum.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Glutamine synthetase (RC 6.3.1.2) (Glutamate--ammonia ligase)
                                                                                                                                                                                  DB 1; Length 439;
                                                                                                                                                                                                          73; Mismatches 209; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLKESKMLNKTFGEKLILHYVNAANVEINEFSKOVTDWELNQ 449
                                                                                                                   A -> G (IN REF. 1).
A -> R (IN REF. 1).
S -> T (IN REF. 1).
; ABE3E674BD2F2359 CRC64;
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                                                                                                                                                                                 Query Match 20.2%; Score 480; Best Local Similarity 29.9%; Pred. No. 1 Matches 138; Conservative 73; Mismatch
InterPro; IPR004809; GlnA.
InterPro; IPR001637; GlnA.adenyltn
Pfam; PP00120; gln-synt; 1.
ProDom; PP03951; gln-synt_N; 1.
ProDom; PP03951; gln-synt_N; 1.
ProDom; PP001057; Gln_synt_C; 1.
IIGRFAM9; TIGR00653; GlnA; 1.
PROSITE; PS00180; GLNA_1; 1.
PROSITE; PS00181; GLNA_ATP; 1.
Ligase; Complete proteome. A -> CONFLICT 204 204 A -> CONFLICT 386 386 S-> SEQUENCE 439 AA; 50035 MW; ABE:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 IMQQIERLANLKIKGL----FASELEFNLFNETYKSASQKHWKNLKTAQPHHQMMNISA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 TDLGENARRDMTLALEEMGFEIEASHHEVAEGÖNEIDFKYGDALTTADNIMTFKLVVKSI 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLNPYLAFSAIIAAGISGIEEKLELPPPASGNVY-----NDKELPEFPNSLQNATHLL 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
   CONTROLLED
                                 BY ADENYLATION. THE FULLY ADENYLATED ENZYME COMPLEX IS INACT: SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       392 392 AMP (UNDER CONDITIONS OF ABUNDANT GLUTAMINE) (BY SIMILARITY).
443 AA; 49682 MW; EDE5BF44495151FC CRC64;
                                                                                                                            -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
-!- CAUTION: Was originally thought to originate from C.acetobutylicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KESKMLNKTFGEKLILHYVNAANVEINEFSKQVTDWELNQGFNRY 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001691; GLN synth.
InterPro; IPR001691; GLN synth.
InterPro; IPR001637; GlnA.
InterPro; IPR001637; GlnA.
Pfam; PF00120; gln-synt; J.
Pfam; PF00120; gln-synt; N.
ProDom; PD001057; Gln-synt C; 1.
ProDom; PS00180; GlnA; 1.
PROSITE; PS00180; GLNA 1; 1.
PROSITE; PS00181; GLNA 1; 1.
PROSITE; PS00182; GLNA ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.6%; Score 466; DB 1; 28.0%; Pred. No. 1.4e-29;
REGULATION: THE ACTIVITY OF THIS
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Matches 130; Conservative
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216 KLVVKTIARKHGLHATFMAKPVHGINGSGMHCNMSL-FTEDGANAFADPTGDMGLSDVAH 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MIITYDELNNL--IRNGKID-----TVVLACVDMQGRLMGKRLTGRHFLGLDQKK 48
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                                                                            ELRIGGADLNPYLAFSAIIAAGISGIEEKLELPPPASGNVY--NDKE-----LPEFPNSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAINE-SOM 1537 / PS;
MEDLINE-90139872; PubMed=2575777;
Possot O., Sibold L., Aubert J.-P.;
"Nucleotide sequence and expression of the glutamine synthetase structural gene, glub, of the archaebacterium Methanococcus voltae.";
Res. Microbiol. 140:355-371(1989).
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                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS)
                                                                                                                                                                                                                                            395 HNAVKALPEDIIVTEALGEHVLVNFVEAKRIEWASYAQFVSQWEIDNYLELY 446
                                                                                                                                                                                                                     403 ONATHLLKESKMLNKTFGEKLILHYVNAANVEINEFSKOVTDWELNQGFNRY 454
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    -!- SUBCELLULAR LOCATION: Cytoplasmic.
    -!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanococcaceae; Methanococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          446 AA; 50199 MW; 95449E4DE8542690 CRC64;
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InterPro; IPR004809; GlnA.
InterPro; IPR001637; GlnA adenyltn.
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Pfam; PF03951; gln-synt_N; 1.
ProDom; PD001057; Gln_synt_C; 1.
TTGPPAMA: TIGR00653; GlnA; 1.
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PROSITE; PS00181; GLNA ATP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methanococcus voltae.
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HSSP; P06201; 1LGR.
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142; Conserv
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E. Best Local'S
Matches 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 KHGVREMAEQSGMVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLAR 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MIITYDELNNLIRNGKIDTVVLACVDMQGRLMGKRL--TGRHFLGLDQKKISISTFVYAV 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26
                                                                                                                                                                                                                                                                                                                      Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
lectis sap. lactis IL1403.";
Genome Res. 11:731-753(2001).
-!- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIEGIAGGGYEISSVDTGYSDCHLCADLNSLHLLPWSE-----GAVLAISNPHNFVTSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QWMNISASSGIETFWRSVRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTMADRHIIA
                                                                                                                                                                      Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- ENZYME REGULATION: DOES NOT SEEM TO BE REGULATED BY ADENYLATION -!- SUBUNIT: Oligomer of 12 subunits arranged in the form of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hexagons (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        446 AA; 49693 MW; COA953D5341AD5CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2e-29;
                      446 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.5%; Score 464; 29.0%; Pred. No. 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, P06201; 1LGR.
InterPro; IPR001691; GLN synth.
InterPro; IPR004809; GlnA.
InterPro; IPR001637; GlnA_adenyltn.
                      PRT;
                                                                                                                                                                                                                                                                             STRAIN=1L1403;
MEDLINE=21235186; PubMed=11337471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00120; gln-synt, I.
Pfam; PP00391; gln-synt, N; 1.
ProDom; PD001057; Gln synt C; 1.
TIGRFAM8; TIGR00653; GlnA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE006449; AAK06298.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00180; GLNA_1; 1.
PROSITE; PS00181; GLNA_ATP; 1.
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                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                   NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           L-glutamine.
                      LACLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ligase; Co
SEQUENCE
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                      GLNA LAC
Q9CDL9;
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Matches 134; Conservative
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                                                                                                                                                                                                                                                                                                                                   L-glutamine.
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VARIĀNT
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VARIANT
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 --VEIEDSDMVLKPDLSTLSVLPWRPSEKSVARIICDV 102
                                                                  103 YRKNGKPF-EGDPRGCLKRV-----LAEFKEEFKGEYFVGPEPEFFILKNENGK--- 150
                                                                                                                                                 196 GQHEVDFKYDNAVKTADSVITFKTTIKTLAKQSGVLATFMPKPFFGMNGSGMHCNQSIWL 255
                                                                                                                                                                                                                              327 CWAIDNRTSAFRLCNSKSEGINVELRIGGADLNPYLAFSAIIAAGISGIEEKLELPPPAS 386
                                                                                                                                                                                                                                                                                       ---------WVPGDDAGYFELEPLDEGNDLRRNIVFALENLGFHVEASHHEVAP 195
                                                                                                                                     208 SQHELNFVPADPLTMADRHIIAKHGVREMAEQSGMVATFMAKLSSTALGNACHIHMSL-Q 266
                                                                                                                                                                                  DAETEKNAFYDQNDEYGMSTLARNWIAGLLKYVPEATYFFASYINSYKRLQPLTFAPTKC 326
                                                                                                                                                                                                                                                                          GNVY------NDKELPEFPNSLQNATHLLKESKMLNKTFGEKLILHYVNAANVEINEFS 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence of the Bacillus subtilis glutamine synthetase gene region.";
Gene 71:257-265(1988).
                                                                                                                                                                                                                                           1S1STFVYAVT1EG1AGGGYE1SSVDTGYSDCHLCADLNSLHLLPW--SEGAVLA1----
                                             --SNPHNFVTSEPLFCSPRVILMQQIERLANLK--LKGLF--ASELEFNLF-NETYKSAS
                                                                                       QKHWKNLKTAQPHHQWMNISASSGIE------TFMRSVRNKLEEAGILMEATHPEFLP
                                                                                                                                                                                              DG---KPSFYDENNAHQLSDICLSYIGGILEHTKALVSVTNPTVNSYKRLVPGYEAPVNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakano Y., Tanaka E., Kato C., Kimura K., Horikoshi K.; "The complete nucleotide sequence of the glutamine synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borchert S., Klein C., Piksa B., Hammelmann M., Entian K.D.; "Sequencing of a 26 kb region of the Bacillus subtilis genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strauch M.A., Aronson A.I., Brown S.W., Schreier H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                     443 AA
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MEDLINE=89138001; Pubmed=2906311;
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                      ---SSIEGF----
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433 TAVTDWE----FNKY 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                      440 KOVTDWELNQGFNRY
                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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Submitted (FEB-1997)
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01-NOV-1995 (
28-FEB-2003 (
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P12425;
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Choi S.K., Codani J.J., Connerton I.F., Capuano V., Carter N.M., RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Benizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Aridser P., Galser P., Galizzi A., Galleron N., Rabins S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guiseppi G., Guy B.J., Hagea K., Halo M. F., Itaya M., Jones L., Alloris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Rabina A., Lardinois S., Lauber J., Lazarvita C., Rasarvita K., Lapidus A., Lardinois S., Lauber J., Lazarvita C., Rabina M., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Rabaro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Rasero V., Pohl T.M., Portetelle D., Porwollik S., Schfone F., Schleich S., Schroeter R., Scoffone F., Schleich S., Schroeter R., Satie Y., Rasactott A., Yaraka K., Satot V., Uchiyama S., Vandenbol M., Vannier F., Vassactott A., Vannier R., Wadler E., Wedler H., Weitzenegger T., R. Wipat A., Yamanotto H., Yamane K., Yashikawa H., Parkma H., Vannier F., Vassactium Bacillus R., Nahikawa H.F., Zungtein E., Yoshikawa H., Danchin A., R., Selliss, R., Waller E., Wedler E., Wedler H., Weitzenegger T., R., Wipat A., Yamana K., Yashikawa H.F., Zungtein B., Yashikawa H., Parkma H., Vannier F., Vashikawa H., Parkma K., Yoshikawa 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MODIFICATION AND NOT SUBJECT TO FEEDBACK INHIBITION.
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-!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- ENZYME REGULATION: NOT REGULATED BY POST-TRANSLATIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indela
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G -> E (IN STRAIN PCI219).

N -> D (IN STRAIN PCI219).

F -> Y (IN STRAIN PCI219).

E2A82D97F3C2D310 CRC64;
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Pred. No. 1e-27;
1; Mismatches 200;
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PROSITE; PS00181; GLNA ATP; 1.
PROSITE; PS00182; GLNA ADENYLATION; 1.
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InterPro, IPR004809, GlnA.
InterPro, IPR001637, GlnA_adenyltn.
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Pfam; Pr003951; gln-synt; N; I.
ProDom; PD001.057; Gln synt C; I.
TIGRFAMS; TIGR00653; GlnA; I.
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EMBL; D00854; BAA00730.1; -.
EMBL; U66480; AAB41080.1; -.
EMBL; Z99113; CAB13630.1; -.
PIK; JT0392; AJBSQS.
HSSP; P06201; 1LGR.
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28.2%;
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                               99 -DGTPFEGDPRNNLKRILKEMEDLGFSDFNLGPEPEFFLFKLDEKGE------PTLEL 149
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                                                           VYAVTIEGIAGGGYEISSVDTGYSDCHLCADLNSLHLLPWS--EGAVLA----ISNPHNF 108
                                                                                                                                                                                                                                                                                                                          286 TLARNWIAGLLKYVPEATYFFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCNSKSE 345
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 54
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                                                                                                                                                                                                                                                                                210 IQTFKLVVKTIARKHGLHATFMPKPLFGVNGSGMHCNLSL--FKNGVNAFFDENADLQLS
                                                                                                                                                                                                                                                                                                                                              -----MGKRLTGRHFLGLDQKKISISTF
                                                                                           49 ---VMFDGSSIEGF----VRIEESDMYLYPDLNTFVIFPWTAEKGKVARFICDIYNP---
                                                                                                                           109 VTSEPLFCSPRVILMQQIERLANLKLKGL-PASELEFNLFNETYKSASQKHWKNLKTAQP
                                                                                                                                                                                             HHQ--WMNISASSGIETFMRSVRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTMADR
                                                                                                                                                                                                                                                           HIIAKHGVREMAEQSGMVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMS
                              4 TREDIEKLVKEENVKYIRLQFTDILGTIKAVEIPVSQLGK-----ALDNK----
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-!- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stranden A.M., .Roos M., Berger-Bachi B.; "Glutamine synthetase and heteroresistance in methicillin-resistant Staphylococcus aureus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNSLONATHLLKESKMLNKTFGEKLILHYVNAANVEINEFSKOVTDWELNQGFNRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi Magai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase)
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SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus.
Bacteria, Firmicutes; Bacillales; Staphylococcus
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TYDELNNLIRNGKIDTVVLACVDMOGRL--
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STRAIN=BB270 / AS63;
MEDLINE=97302513; Pubmed=9158760;
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 VILMQQIERLANLKLKGL-FASELEFNLFNETYKSASQKHWKNLKTAQPHHQ-----WM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TITYDELNNLIRNGKIDTVVLACVDMQGRLMGKRLTGRHFLGLDQKKISISTFVYAVTIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 AGLLKYVPEATYFFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCNSKSEGINVELR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353 IGGADLNPYLAFSAIIAAGISGIEEKLELPPPASGNVY--NDKE-----LPEFPNSLQNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glutamine synthetase (Erc 6.3.1.2) (Glutamate--ammonia ligase) (GS).
GLNA OR SAV1310 OR SA1150.
Staphylococcus aureus (strain Nuso / ATCC 700699), and
Staphylococcus aureus (strain Nuso).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TAXID=158878, 158879;
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                                                                                                                                                                                                                                                                                                                                                                         446 AA; 50840 MW; 81713EE654D7E7E6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             92; Mismatches 211;
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EMBL; ATGATO.; CAA54030.1; -.
PIR; TS1803; TS1803.
HSSP; P06201; 1LGR.
INTERPO: IPR001691; GLN synth.
INTERPO: IPR004809; GINA.
INTERPO: IPR001637; GINA.
INTERPO: IPR001637; GINA.
                                                                                                                                                                                                                                              Pfam; PF00120; gln-synt; T.
Pfam; PP00351; gln-synt, N. 1.
ProDom; PD001057; gln synt C; 1.
IGRPAMs; IIGR00653; GlnA; I.
                                                                                                                         EMBL; AP004826; BAB95057.1; -.
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PROSITE; PS00181; GLNA_ATP; 1.
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SEQUENCE
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Query Match
Best Local Similarity 28.34
Matches 133, Conservative
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                                                                                                                                                                                                       -i- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate L-glutamine.
         SEQUENCE FROM N.A.
STRAINSWING) / ATC7 700599, and N315;
MEDLINE=21311952; PubMed=11418146;
MEDLINE=21311952; PubMed=11418146;
MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kannehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba 'Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
                                                                                                                                                                                                                                     -!- SUBUNIT: Oligomer of 12 subunits arranged in the form of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 446;
                                                                                                                                                                                                                                                  hexagons (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.8%; Score 423; DB 1; Length 44 ilarity 28.5%; Pred. No. 3.8e-26; Conservative 82; Mismatches 169; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P06201; 1LGR.
InterPro; IPR001691; GLN_synth.
InterPro; IPR004809; GlnÄ.
InterPro; IPR001637; GlnÄ_adenyltn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00120; gln-synt; T. Fram; PF03951; gln-synt, N; 1. ProDom; PD001057; gln synt_C; 1. TIGRFAMS; TIGR0653; GlnA; 1. PROSITE; PS00180; GLNA_1; 1. PROSITE; PS00181; GLNA_AFP; 1. Ligase; Complete proteome. SEQUENCE 446 AA; 50854 MW; FF91
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP003361; BAB57472.1; -. EMBL; AP003133; BAB42404.1; -.
                                                                                                                                                                                         Lancet 357:1225-1240(2001).
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PIR; H89905; H89905.
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Matches 112; Conserv
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CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADENYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93073974; PubMed=1359838;
Ishino Y., Morgenthaler P., Hottinger H., Soell D.;
"Organization and nucleotide sequence of the glutamine synthetase
(glnA) gene from Lactobacillus delbrueckii subsp. bulgaricus.";
Appl. Environ. Microbiol. 58:3165-3169(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- ENZYME REGULATION: DOES NOT SEEM TO BE REGULATED BY ADENYLATI
-:- SUBUNIT: Oligomer of 12 subunits arranged in the form of two
hexagons (By similarity).
-:- SUBCELLULAR LOCATION: Cytoplasmic.
-:- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 445;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lactobacillus delbrueckii (subsp. bulgaricus).
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          445 AA; 50133 MW; A57A9E11ABAF87E8 CRC64;
                                        422 KLILHYVNAANVEINEFSKQVTDWELNQGFNRY 454
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InterPro, IPR004809; GlnA.
InterPro, IPR001637; GlnA_adenyltn.
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Pfam, PF03951; gln.eynt_N, 1.
ProDom, PD0010051, Gln.eynt_C; I.
TIGRFAMS; TIGR00651; GlnA; I.
PROSITE; PS00180; GLNA_1; I.
PROSITE; PS00181; GLNA_1; I.
                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seqt
28-FEB-2003 (Rel. 41, Last anno
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28.3%;
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                      217
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                                                                                                                                                                                                       YEDWASEDEGAKCRREIVETLEKLGFRVEAAHHEVGDGQQEIDFRFDNALATADKLQTFK
                                                  HGVREMAEQSGMVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLARN
                                                                        WIAGLLKYVPEATYFFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCNSKSEGINVE
                                                                                                                                                   FLNGILEHARAITCVANPTVNSYKRLIPGFEAPVYISWASRNRSPMVRIPNANEVGTRLE
                                                                                                                                                                                      LRIGGADLNPYLAFSAIIAAGISGIEE-KLELPPPASGNVY--NDKELPE-----FPNSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakano Y., Kato C., Tanaka E., Kimura K., Horikoshi K.;
"Nucleotide sequence of the glutamine synthetase gene (glnA) and its
upstream region from Bacillus cereus.";
J. Blochem. 106:209-215(1989).
-!- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate
                                                                                                                                                                                                                                                        452
                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENZYME REGULATION: NOT REGULATED BY POST-TRANSLATIONAL MODIFICATION AND NOT SUBJECT TO FEEDBACK INHIBITION. SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF
                                                                                                                                                                                                                                                    ONATHLLKESKMLNKTFGEKLILHYVNAANVEINEFSKOVTDWELNQGFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Firmicutes; Bacillales; Bacillaceae; Bacillus.
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InterPro; IPR001691; GLN synth.
InterPro; IPR001637; GlnA adenyltn.
Pfam; PP03921; gln-synt; I.
ProDom; PD001057; Gln synt, I.
ProDom; PD001057; Gln synt, C; I.
ProSTEP, PS00180; GLNA; I.
PROSITE; PS00180; GLNA; I.
PROSITE; PS00181; GLNA ATP; I.
PROSITE; PS00182; GLNA_ADENYLATION; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=IFO 3131;
MEDLINE=90036764; PubMed=2572584;
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01-NOV-1995 (Rel. 32, Last seq
15-DEC-1998 (Rel. 37, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D00513; BAA00403.1; -. PIR; JU0075; AJBSQU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus cereus.
Bacteria; Firmic
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SEQUENCE
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                                                                                                                                                                                                                                                                           63 IAGGGYEISSVDTGYSDCHLCADLNSLHLLPWS--EGAVLAISNPHNFVTSEPLFCSPRV 120
                                                                                                                                                                                                                                                                                                                      F-----VRIEESDMYLYPDLDTWVIFPWTAEKGKVARLICDIYNADGTPFEGDPRN 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 HGVREMAEQSGMVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLARN 290
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                                                                                                                                                                                                       4 TKEDIFRLAKEENVKYIRLQFTDLLGVIKNVEIPVSQLTKALDNKMMFDGS----SIEG
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                                                                       Gaps
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                                                                   51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
(EC 6.3.1.2) (Glutamate--ammonia ligase)
   Length 443;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404 NATHLLKESKMLNKTFGEKLILHYVNAANVEINEFSKQVTDWELNQGFNRY
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                                                                   Indels
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Archaea; Buryarchaeota; Methanococci; Methanococcales;
Methanococcacea; Methanococcus.
NCBI_TaxID=39152;
17.3%; Score 411.5; DB 1; 26.8%; Pred. No. 3.1e-25; ive 82; Mismatches 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Bacteriol. 181:256-261(1999).
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15-DEC-1998 (Rel. 37, Last seq
30-MAY-2000 (Rel. 39, Last ann
Glutamine synthetase (EC 6.3.1
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                                                                       Conservative
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                                                                Matches 126;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 PRSRLKAILEELKK-EMNGEYFVGPEPEFFLLKR--------DPHNPHRWVP 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIIAKHGVREMAEQSGMVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEY-GM 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STLARNWIAGLLKYVPEATYFFASYINSYKRLOPLTFAPTKCCWAIDNRTSAFRLCNSKS 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279 SETCLSYIÁGILSHAKALVAITNPTVNSÝKRÍVÞGYEAÞVNIAWANKNRSAIIRVPAARG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGINVELRIGGADLNPYLAFSAIIAAGISGIEEKLELPPPASGNVYNDKE-----LPE 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----NISASSGIETFMRSVRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTMADR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRVILMOQIERLANLKLKGLF - - ASELEFNLFNETYKSASOKHWKNLKTAQPH - - HQWM -
                               CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS)
GLNA OR WTH1570.
Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 454;
                                                                 L-glutamine.
SUBCELLULAR LOCATION: Cytoplasmic (Potential).
SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   398 FPNSLQNATHLLKESKMLNKTFGEKLILHYVNAANVEINEFSKQVTDWE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.8%; Score 398.5; DB 1; 28.9%; Pred. No. 3.5e-24; cive 65; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILERPING JANUARY DERONGEDI, GLN SYNTH.

INTERPRO, IPROOLEGI, GLN Adenyltn.

PERNO 1 PROOLEGI, GLN Adenyltn.

PERNO 1 PROOLEGI, GLN Adenyltn.

PERNO 1 PROSESI, GLN SYNT, I.

PROSITE; PSOOLEGI, GLN SYNT, C.

TICRERAM; TICREOGESI, GLN ALI, I.

PROSITE; PSOOLEGI, GLNA ALI, I.

LIGARE; COMPLETE PSOOLEGI, GLNA ALI, I.

LIGARE; COMPLETE PSOOLEGI, GLNA ALI, I.

LIGARE; COMPLETE PSOOLEGI, GLNA ALI, I.

SEQUENCE 454 AA; 51398 MW; 3222CB
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Science 273:1058-1073(1996)
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es 118; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P06201; 1LGR.
TIGR; MJ1346; -
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYDVLEKGVYFDGSSIEGFVSIESSDMMLKPDLKTLSVLPWRPTEKSVARVICDVYTTNG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :| | : : : | | | : : : | | | 107 KPFEGDPRGCIKRVLAKF-DEELGGEFFVGPEPEFFILKEDACGS----WVPADDA---- 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 SYVAĞILDHAKSIVAVTNPTVNSYKRLVPĞYEAPVNIAWANSNRSAIVRVPAPRĞKĞTRI 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELRIGGADLNPYLAFSAIIAAGISGIEEKLELPPPASGNVYNDKE-----LPEFPNSL 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPLFCSPRVILMQQIERLANLKLKGLF--ASELEFNLFNETYKSASQKHWKNLKTAQPHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QWMNISASSGIETFMRSVRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTMADRHIIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 NWIAGLLKYVPEATYFFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCNSKSEGINV
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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
STRAIN=963399; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Phurmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KHGVREMAEQSGMVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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01-NOV-1997 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           403 QNATHLLKESKMLNKTFGEKLILHYVNAANVEINEFSKQVTDWELNQ 449
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                                                                                                                                                                                                                                                                                                                                                                DDE984106651122A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
16.9%; Score 400.5; DB 1;
Best Local Similarity 28.3%; Pred. No. 2.3e-24;
Matches 115; Conservative 70; Mismatches 199;
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                           InterPro; IPR001691; GLN synth.
InterPro; IPR004809; GlnA.
InterPro; IPR001637; GlnA_adenyltn.
                                                                                                                     Pfam, PF00120; gln-synt; I.
Pfam, PF03951; gln-synt, N. 1.
ProDom, PD001057; gln-synt C; 1.
TIGRFAMS; TIGR0653; GlnA; 1.
PROSITE; PS00180; GlNA I; 1.
PROSITE; PS00181; GLNA AFP; 1.
                                                                                                                                                                                                                                                                                                                                                                   446 AA; 49421 MW;
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Methanococcus jannaschii.
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Q60182;
01-NOV-1997 (
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SEQUENCE
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225 220

Gaps

47;

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337 DPSCNPYLAFAAMLEAGMNGIQNKIDPGEPTEIDVY-EKSMSELREMGIETLPSSLWEAY 395
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                        GLN2 MYCTU
Q10378;
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                                                                                                                                                                                                                                                                                                         ligase 2).
                                                                                               396
                                                         407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 PVDQGTDFRRKIVMDLEALNFDVEVSHHEVAPQQHEIDFKFDKALKTADAVITFKQAIKA 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 PRVILMQQIERLANLKLKGLFASELEFNLFNETYKSASQKHWKNLKTAQPHH--QWMNIS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 ASSGIETFMRSVRNKLEEAGILMBATHPEFLPSQHELNFVPADPLTMADRHIIAKHGVRE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 IVDKIGYMVTFMPKPFFGENGSGMHCHQSLFKDGE---NVFYDPDTFTQLSEALYFIGG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLKYVPEATYFFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCNSKSEGINVELRIG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 GADLNPYLAFSAIIAAGISGIEEKLELPPPASGNVYNDKELPE-----FPNSLQNAT 406
                                                                                                                                            Smith D.R., Doucette-Stamm. L.A.; Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N., "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 MAEQSGMVATFMAKLSSTALGNACHIHMSL-QDAETEKNAFYDQNDEYGMSTLARNWIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372 AMP (UNDER CONDITIONS OF ABUNDANT GLUTAMINE) (BY SIMILARITY)
50248 MW, B907928AADB960A6 CRC64;
Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales,
Methanobacteriaceae; Methanothermobacter.
NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DB 1; Length 442;
6.3e-24;
                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.6%; Score 395; DB 1; Length 442;
28.5%; Pred. No. 6.3e-24;
.ive 71; Mismatches 189; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, P06201; 1LGR.
INLEXPRO, IPR001691; GLN synth.
INLEXPRO; IPR004809; GlnÄ.
INLEXPRO; IPR001637; GlnA_adenyltn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001637; GlnA adenyltn Pfam; PF00120; gln-synt; I. Pfam; PR03951; gln-synt N; 1. ProDom; PD01057; Gln synt C; 1. TIGRFAMs; TICR00653; GlnA; 1. PROSITE; PS00180; GLNA 1; 1. PROSITE; PS00181; GLNA ATP; 1.
                                                                                                           STRAIN=Delta H;
MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000917; AAB86044.1; -.
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Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ligase; Complete proteome
BINDING 372 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     442 AA;
                                                                                                                                                                                                                                                                                                                                                                 L-glutamine.
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Best Local
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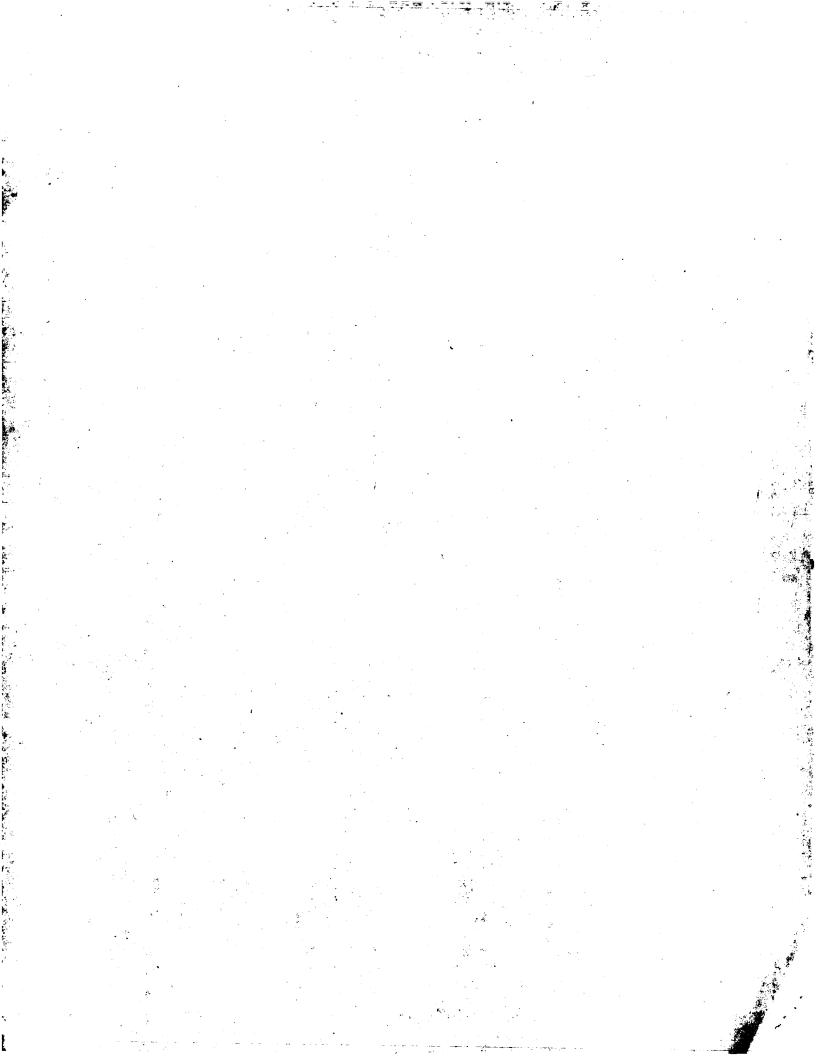
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Earbenter D., Hickey E.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laboratory strains."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. -!- CATALYTIC ACTIVITY: ATP ^+ L-glutamate ^+ NH(3) = ADP ^+ phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandram M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Deciphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L-glutamine.
-!- SUBUNIT: Oligomer of 12 subunits arranged in the form of two
                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Probable glutamine synthetase 2 (EC 6.3.1.2) (Glutamate--ammonia
                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hexagons (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
                        HALEEDDVIKGALGGHVYEKFMEIKHREWDDYRVFKYELER 438
HLLKESKMLNKTFGEKLILHYVNAANVEINEFSKQVTDWELNQ 449
                                                                                                                                                                                                                                                                                                 GLNA2 OR RV2222C OR MT2280 OR MTCY427.03C OR MTCY190.33C.
                                                                                                                                                 446 AA
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InterPro; IPR001631; GLN synth.
InterPro; IPR004691; GlN adenyltn.
Pfam; PP00120; gln synt; I.
Pfam; PF03951; gln synt; I.
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MEDLINE=98295987; PubMed=9634230;
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EMBL; AE007073; AAK46565.1; -.
PIR; B70776; B70776.
HSSP; P06201; 1LGR.
TIGR; MT2280; -.
                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
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tches 137; Conservative
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EWELERYF
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NCBI_TaxID=29292;
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                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                Query Match
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Q9UY99;
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GLNA_PYRAB
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                                                                                                                                                                  ----SPRVILMQQIERLANLKLKGLFASELEFNLFNETYKSASQKHWKNLKT
                                                                                                                                                                                                                                                          165 AQPHHQWMNISASSGIETFWRSVRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTMAD
                                                                                                                                                                                                                                                                          150 PVDNAGYFDQAVHDSALNFRRHAIDALEFWGISVEFSHHEGAPGQQEIDLRFADALSMAD
                                                                                                                                                                                                                                                                                                                225 RHIIAKHGVREMAEQSGMVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGM
                                                                                                                                                                                                                                                                                                                               STLARNWIAGLLKYVPEATYFFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRL---CN
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                                                                                                                                                                                                                                                                                                                                                                                                                          SKSEGINVELRIGGADLNPYLAFSAIIAAGISGIEEKLELPPPASGNVYN-----DKE
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrococcus kodakaraensis.
Archaea: Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
Thermococcus.
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=KDD1;
MEDLINE=97316461; PubMed=9172372;
MEDLINE=97316461; PubMed=9172372;
MEDLINE=97316461; PubMed=9172372;
"Characterization of recombinant glutamine synthetase from the hyperthermophilic archaeon Pyrococcus sp. scrain KOD1.";
Appl. Environ. Microbiol. 63:2472-2476 (1997).
-i- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             388 YRELPSSLDSALRAMEASELVAEALGEHVFDFFLRNKRTEWANYRSHVTPYEL 440
                                                                                                                       45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase)
                                                                                              Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L-glutamine.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
                                                                                                                      Indels
ProDom; PD001057; Gln synt_C; 1.
TIGREAMS; TIGR00653; GlnA; 1.
PROSITE; PS00180; GLNA_1; FALSE NEG.
PROSITE; PS00181; GLNA_ATP; FALSE NEG.
Ligase; Multigene family; Complete proteome.
SEQUENCE 446 AA; 49607 MW; 86F163FD017829DD CRC64;
                                                                                           Query Match 16.6%; Score 393.5; DB 1; Best Local Similarity 28.1%; Pred. No. 8.5e-24; Matches 116; Conservative 77; Mismatches 175;
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48 DGVSFDGSSIPGFE-GIEDSDLIPKADPSTYAEIPW-EG----IGRVYGYIYKGDEPYQA 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 HIIAKHGVREMAEQSGMVATFMAKLSSTALGNACHIHMSL-QDAETEKNAFYDQNDEYGM 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 SGARIĖYRCPDPSANPYLALAGILMVGLDGIKKKVEPDSYVETNVYEMDDAERERLGIDT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 IVSFKHVVKAVAELHGYYATFMPKPIYGFPGNGMHLHISLWKDGE---NVFIGED---GL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 EGIAGGGYEISSVDTGYSDCHLC--ADLNSLHLLPWSEGAVLAISNPHNFV--TSEPLFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 SASSGIETFM----RSVRNK----LEEAGILMEATHPEFLPSQHELNFVPADPLTMADR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 DELNNLIRNGKIDT-----VVLACVDMQGRLMGKRLTGRHFLGLDQKKISISTFVYAVTI
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Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
(EC 6.3.1.2) (Glutamate--ammonia ligase) (GS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90;
                                                                                                                                                                                                                                                                                                                                    ABUNDANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78; Mismatches 183; Indels
                                                                                                                                                                                                                                                                                                                                 362 362 AMP (UNDER CONDITIONS OF AL GLUTAMINE) (BY SIMILARITY) 443 AA; 50259 MW; 9426DCCFEEF18168 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 391; DB 1;
Pred. No. 1.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      439 AA
                                           InterPro; IPR001691; GLN synth.
InterPro; IPR004809; GlnA.
InterPro; IPR004809; GlnA.
InterPro; IPR001637; GlnA adenyltn.
Pfam; PF00120; gln-synt; 1.
Pfam; PF001951; gln-synt; 1.
IGRPAMS; TIGR00653; GlnA; 1.
PROSITE; PS00180; GLNA_1; 1.
PROSITE; PS00181; GLNA_1; 1.
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16-OCT-2001 (Rel. 40, Last seq
15-SEP-2003 (Rel. 42, Last ann
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28.1%;
D86222; BAA20530.1;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 SDLIFKADPDTYVEVPWDN-----VARVYGYIYKDGKPYGADPRGVLKRVIEKLAEMGIK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 RLOPLTFAPTKCCWAIDNRTSAFRLCNSKSEGINVELRIGGADLNPYLAFSAIIAAGISG 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 GLFASELEFNLFNETYKSASQKHWK-NLKTAQPHHQWMNISASSGIETFMRSVRNKLEEA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79
                                 Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O., Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C., Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P., An integrated analysis of the genome of the hyperthermophilic archaeon Pyrococcus abyssi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 PGNGMHLHISLW--KEGENIF---KGEEGLSETALHFIGGLLKHAKALTAITNPTVNSYK
                                                                                                                                 Mol. Microbiol. 47.1495-1512(2003).
-!- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate +
L-glutamine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 VVLACVDMQGRLMGKRLTGRHFLGLDQKKISISTFVYAVTIEGIAGGGYEISSVDTGYSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 VQLIFVDINGMPKGMEIPASRL----QEAIE-----DGISFDGSSVPGFQ-GIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 CHLC--ADLNSLHLLPWSEGAVLAISNPHNFV--TSEPLFCSPRVILMQQIERLANLKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AYIGPEPERYLEK---KNGS---WELEIPDVGGYFDILTLDKAKDÍK---REIAEYMPSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 GILMEATHPEFLPSQHELNFVPADPLTMADRHIIAKHGVREMAEQSGMVATFMAKLSSTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMP (UNDER CONDITIONS OF ABUNDANT
                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.4%; Score 389.5; DB 1; Length 4: 28.0%; Pred. No. 1.7e-23;
tive 73; Mismatches 195; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLUTAMINE) (BY SIMILARITY).
62CCFD3970A98AF0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----KLILHYVNAANVEINEFSKQVTDWELNQGF 451
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ24828; CAB50513.1; -. PRR; CT5009; CT5009. HSSP; P06201; LLGR.
INCEMPRO; IPR001691; GLN synth.
INCEMPRO; IPR001691; GLN adenyltn. Pfean; PP00120; Gln-synt, I. Pfam; PP03951; Gln-synt, I. Propom; PP001057; Gln-synt, I. PROSITE; PS00180; GLNA.1; I. PROSITE; PS00180; GLNA.1; I. PROSITE; PS00180; GLNA.1; I. Ligase; Complete proteome.
BINDING 358 358 AMP (UND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             439 AA; 49742 MW;
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Search completed: December 17, 2003, 22:43:22 Job time : 14 secs



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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

em_gss_phg:* em_gss_vrl:* gb_gssl:* hum: * gb_htc:* gb_htc:* gb_est3:* gb_est4:* gb_est5:* em_est5::* inv:* *:uld vrt:* fun: #:8nm em_gss_pro:* em_gss_rod:* mam: em_estba:* em_esthum:* em_estin:*
em_estmu:*
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	,	Description	370989 ra53cl	72 ra73h03.	375 ru99e0	245	184 PUHHO6	873 PUHFA2	035 PUBMO8	175 BJ3471	738 PUBFS6	214 PUBDI1	241 BJ3582	680 rockef	63 AU039163	227 PUHMO4	677 TDGDR4	742 Fgr 5	122 PUBCRB	29 M32 WDe	159 PUHDF85	494 PUBMJ14	16	9	BZ558114 pacs1-60	0 6	860	25	83	73,	1/1 MES120/-	282 Zea mays	62 EST26	40402 WHE0483	58011 BJ26801	33379 T047C06	51228 FgrN_5_	81957 WHE3027	82096 WHE3028	CD452699 WHE1119 H	202/0 6041512	/6033 CT_EMD_
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ALIGNMENTS

AW870989 S01 bp mRNA linear EST 10-MAY-2001	ra53c11.yl Bird-Rao Meloidogyne incognita J2 Meloidogyne incognita cDNA 5. similar to TR:088070 088070 PUTATIVE GLUTAMINE SYNTHETASE.	AW870989	AW870989.1 GI:8005042		Meloidogyne incognita (southern root-knot nematode)	Meloidogyne incognita	Eukaryota, Metazoa, Nematoda, Chromadorea, Tylenchida, Tylenchina,	Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
AW8	ra5.	AW8	AW8	EST.	Mel	Mel	Buk	ľyľ
RESULT 1 AW870989 LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM		

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/dev_stage="enriched for 2nd stage juveniles"
/dev_stage="enriched for 2nd stage juveniles"
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/note="vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; ...
Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
1 (Dasea 1 to 442).
McCarter, J. (Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylle, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, B., Bennett, J., Franklin, C., Tagaraeishvili, R., Rohko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Sreptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Uackson, Y., Cardenae, M., McCann, R., Waterston, R. and
                                                                                                                                                                                                                                                                ra73h03.yl Bird-Rao Meloidogyne incognita J2 Meloidogyne incognita 72 Meloidogyne incognita 72 Meloidogyne incognita 7. mRNA sequence.
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The library was constructed by Uma Rao and David Bird
(david bird@ncsu.edu) at North Carolina State University. DNA
Sequencing by: Washington University Genome Sequencing Center St.
Louis.
Trace considered overall poor quality
                                                          TyrValAsnAlaAlaAsnValGluIleAsnGluPheSerLysGlnValThrAspTrpGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
Context: McCarter JP
Context: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meloidogyne incognita (southern root-knot nematode)
Meloidogyne incognita
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Mismatches:
Indels:
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                                                                                                                                         454
                                                                                                                                                                         Seg primer: -40RP from Gibco
High quality sequence stop: 1.
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                                                                                                                                      447 LeuAsnGlnGlyPheAsnArgTyr
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Best Local Similarity:
Query Match:
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McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hiller, L., Kucaba, T., Theising, B., Bowers, Y., Glbbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Bird-Rao Meloidogyne incognita J2"
/note="Vector: ZAP express - pBKCMV (Stratagene); Site_l:
EcoRI; Site_2: Xhol; Oligo (dT) primed library. CDNA was
contructed and cloned unidirectionally into the vector
within the 5' EcoRI and 3' Xhol sites. This library was
constructed by Dr. Uma Rao and Dr. David Bird at North
constructed by S g 156 t
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                                                                                                                                                                                                                                                                            Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Uma Rao and David Bird
(david bird@ncsu.edu) at North Carolina State University. DNA
Sequencing by: Washington University Genome Sequencing Center:
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/lab_host="XLORL"
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The Washington Univ. Nematode EST Project, 1999
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Seq primer: -40RP from Gibco
High quality sequence stop: 410.
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/db_xref="taxon:6306"
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This library was generated by cloning cDNAs directionally into
Uni-ZAR(Stratagene) (T3 primer/EcoRi are at the 5'-end and T7/XhoI
ser at the 3'-end). The library was excised inow in pBluescript
SK(+)] and normalized (Bonaldo et al 1996 Genome Research 6:791-806
). Library constructed by Thomas Baum (tbaum@iastate.edu), Iowa
State University, Plant Pathology Department and Jeff McDermott
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Heterodera glycines
Heterodera glycines
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchoidea; Heteroderidae; Martin, J., Wylie, T., Globons, M., Marta, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Globons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steppce, M., Allen, M., Person, B., Swaller, T., Harvey, M., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and
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The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1800
Email: est@watson.wustl.edu
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FEATURES

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/clone lib="Heterodera glycines virgin female" /note="Vector: pBluescript SK+ (Stratagene); Site 1: XhoI; Site 2: ScoRI; This library was generated by cloning cDNAs directionally into Uni-ZAP(Stratagene) (T3 primer/EcoRI are at the 5'-end and T7/XhoI are at the 3'-end). The
                                                                                                                                                                                                                                                                    library was excised [now in pBluescript SK(+)] and normalized (Bonaldo et al 1996 Genome Research 6:791-806). Library constructed by Thomas Baum (tbaum@lastate.edu), Iowa State University, Plant Pathology Department and Jeff MCDermott (jmcderm@lastate.edu)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 TCGTACAAGCGACTGCAGCGGAACAGTTGGGCACCAACAAAAATTTGTTGGACTGTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AsnArgThrSerAlaPheArgLeuCysAsnSerLysSerGluGlyIleAsnValGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 CGTATTGGTGGGGCCGACCTCAACCCGTACTTGGCATTCGCCGCACTGATCGCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 IleSerGlyIleGluGluLysLeuGluLeuProProProAlaSerGlyAsnValTyrAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||||:::|||||| |||||| ||||:::
362 AATTCGGAAATGTTGAAAAGAGCGTTGGGTGAAAATGTTTTACGACACTACAAAAATTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ArgileGlyGlyAlaAspLeuAsnProTyrLeuAlaPheSerAlaIleIleAlaAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           392 AspLysGlu---LeuProGluPheProAsnSerLeuGlnAsnAlaThrHisLeuLeuLys
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93
29
1
1
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Conservative:
Mismatches:
Indels:
organism="Heterodera glycines"
                                                                                   tissue_type="whole organism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                     'mol_type="mRNA"
'db_xref="taxon:51029"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-098-602A-2 (1-454) x CB374375 (1-621)
                                                                                                           /dev_stage="adult"
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                                                                sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.66e-47
506.50
74.85%
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TTTGACAGA 490
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PUBMN15TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa089C06, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                            366 GCACTGATAATGGCGGATATGCATGATCAC---CGCGATTTGCCTTTCTTTTGTGCCCCG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 AlaSerGluLeuGluPheAsnLeuPheAsnGluThrTyrLysSerAlaSerGlnLysHis 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   483 GCCTCCGAATTGGAGTTTCATTTGTTCAGCGAGAGCCAAAAGAGTGCGGGGAAAAGCAA 542
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/clone lib="zM 0.6 1.0 KB"
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CoT selected genemic DNA library"
1 265 c 308 g 150 t
                                                                                      ThrileGluGlyIleAlaGlyGlyGlyTyrGluIleSerSerValAspThrGlyTyrSer 78
                                                                                                                                                                                                       79 AspCysHisLeuCysAlaAspLeuAsnSerLeuHisLeuLeuProTrpSerGluGlyAla 98
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Mitclaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick
WA., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennetzen,J.
Maize Genomics Consortium
TTGTTGAAATGGCGCAAAAAAAAGACAAAATGTCCATGTGCTATTTCCTTGCGATG
                                                                                                                       9712 Medical Center Drive, Rockville, MD 20850, USA
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/strain="B73"
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Location/Qualifiers
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Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Cathy Whitelaw
TIGR
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BZ701245.1 GI:28421092
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Pred. No.:
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Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 315 286 1810
Fax: 315 286 1810
This library was generated by cloning cDNAs directionally into
University Stratagene) (T) primer/ECORI are at the 5'-end and T7/XhoI
are at the 3'-end). The library was excised [now in pBluescript
SK(+)] and normalized (Bonaldo et al 1996 Genome Research 6:791-806
). Library constructed by Thomas Baum (tbaum@iastate.edu), Iowa
State University, Plant Pathology Department and Jeff McDermott
(jpmcderm@iastate.edu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="whole organism"
/dev stage="whole organism"
/dev stage="whole organism"
/dev stage="bhlos"
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/clone_lb="heterodera glycines J4"
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                                                                                                                                                                                           McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Glbbons, M., Ritter, B., Bennett, J., Franklin, C., Taagaredshvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
                                                                                Heterodera glycines
Eukaryota, Metazoa, Nematoda, Chromadorea, Tylenchida, Tylenchina,
Tylenchoidea, Heteroderidae, Heteroderinae, Heterodera.
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Unpublished
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/organism="Heterodera glycines"
/mol_type="mRNA"
/db_xref="taxon:51029"
/eex="mixed"
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High quality sequence stop: 480.
Location/Qualifiers
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  GI:28567385
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                                                           Heterodera glycines
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CB279008.1
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us-10-098-602a-2.rst

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495 AGCGCCGTCACCAACCAGGGGGGGGAACAGTTACAAGCGCCCTGATCCACGGCGGGGGAACAG 436
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Indels:
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae, PACCAD (adae, Panitocideae; Andropogoneae; Zea. 1 (Bases 1 to 825)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Praser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J. Unpublished
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                                                                                                                                                                                                                                              9712 Medical Center Drive, Rockville, MD 20850, Tel: 301-888-5845 Fax: 301-838-0208 Email: whitelaw@tigr.org
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/clone=lb="xm 0.6_1.0 KB"
/note="Vector: pCR4-T0P0; Site_1: 1
COT selected genomic DNA library"
a 258 c 298 g 148 t
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/strain="B73"
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Location/Qualifiers
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TIGR
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                                                  276 CTCGCCGCCGGACTCAAGGGCATCGCCGAGAAGTACGAGCTGCCCGACGACGACGAGGAC 217
                                                                            AsnValTyr------AsnAspLysGluLeuProGluPheProAsn 400
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Bopermatophyta; Bagnollophyta; Lillopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 851)
whitelaw.C.A., Quackenbush.J., Van Aken,S., Utterback,T., Resnick,A., Fraser.C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennetzen,J.
Maize Genomics Consortium
CGCATCGAGGTCCGCAGCCCCGACTCGGCTTGTAACCCCTACCTGACGTTCGCGGTGCTG 277
                         368 IleAlaAlaGlyIleSerGlyIleGluGluLysLeuGluLeuProProProAlaSerGly 387
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/clone=lb="ZM 0.6.1.0 KB"
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CoT selected genomic DNA library"
269 c 308 g 153 t
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Seg primer: TF
Class: sheared ends.
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Fax: 301-838-0208
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PheMetArgSerValArgAsnLysLeuGluGluAlaGlyIleLeuMetGluAlaThrHis 202

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BZ705035 815 bp DNA linear GSS 19-FEB-2003 PUBMO84TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa089N23,
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1 (basea 1 to 815)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J. Unpublished
Trcccccccccacccarcaccccacccacccarcaccarcaccarcacccacccacccarcacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccacccaccaccacccacccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccaccacca
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385 CCGACCGCCGCGACGTGGCGCGAACCGCTCCCGCGCTCATCCGGCTCCTGTAC 326
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9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
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147 TTCCTCCGCAACAAGTGGACCGAGTGGAACGACTACCGCAGCCGGGTCACCCCGTTCGAG
                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
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AUTHORS
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                                                                                                           /db_xxef=rtaxon:4577"
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COT selected genomic DNA library"
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Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1. 815
/organism="Zea mays"
/mol type="genomic DNA"
/strain="B73"
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Dictyostelium discoideum
Eukaryota; Mycetcozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 6 90)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the aggregation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||| :: ||| || || || GGCTGCTCAGGACACTGATTCAATTGTTTAAAAACCGGTAAGAACCTATTC
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                                                                                                                                                                                 BJ347175 Dictyostelium discoideum cDNA linear BJ347175 Dictyostelium discoideum cDNA library, AF BJ347175 GI:19217682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="Aggregation stage"
/clone_lib="Dictyostelium discoideum
110 c 112 g. 262 t 2 ot
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
111 1559-81-6856
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Location/Qualifiers
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us-10-098-602a-2.rst

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1176 bp DNA linear GSS 17-DEC-2002 pace2-164_871.s2 pace2-164 Pseudomonas aeruginosa genomic clone pace2-164_871, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354 GlyGlyAlaAspLeuAsnProTyrLeuAlaPheSerAlaIleIleAlaAlaGlyIleSer 373
                                                                                                          464
                                                                                                                                                                                                                                                                             LysTyrValProGluAlaThrTyrPhePheAlaSerTyrIleAsnSerTyrLysArgLeu 316
                                                                                                                                                                                                                                                                                                                                                                             317 GlnProLeuThrPheAlaProThrLysCysCysTrpAlaIleAspAsnArgThrSerAla 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 ATCCGGCTCCCGCTGTACACGCCGAACAAGGGTCGTCGCGACGCATCGAGGTCCGCGC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGACTCGGCTTGTAACCCCTACCTGACGTTCTCGCGGTGCTGCTGCTGCCGGGCTCAAG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 GGCATCGCCGAGAAGTACGAGCTGCCCGACGAGGACGACGACGTCTGGGCCCTCACC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 TCGGCCGAGCGTCGCACGATGGGCTACACCGAGCTGCCCGGCAGCCTCGCGAGCGCCCAGGCGCTC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  407 HisteuteutysGluSertysMetLeuAsntysThrPheGlyGluLysLeuIleLeuHis 426
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 1176)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Psedomonas aeruginosa library
J. Bacteriol., (2002) In press
AspGlnAsnAspGluTyrGlyMetSerThrLeuAlaArgAsnTrpIjeAjaGjyLeuLeu
                                                                                                                                                                                                               ATCCACGGCGACGACCGACCGCCGCGCACGTGGGGTGGCGCGAACCGCTCCGCGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 AAGGCGATGGAGTCCTCGGAGCTGGTCGGCGAGGCACTCGGCGAGCACTGTTCGACTAC
                                                                        AsnalaCysHisIleHisMetSerLeuGlnAspAlaGluThrGluLysAsnAlaPheTyr
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1. 1176
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
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University of Washington
Box 352145, Seattle, WA 98105-2145, USJ
Tel 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
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Contact: Chris K. Raymond
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BZ569521/c
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DEFINITION
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Class: sheared ends.
Localino/Qualifiers
1. 699
| organism="Zea mays" |
| mol Lype="ganomic DNA" |
| ktrain="B73" |
| clone="Zmanomic DNA" |
| clone="Zmanomic DNA" |
| note="Vector: pCR4-TOFO; Site_1: EcoRI; 0.6-1.0 kb high |
| CoT selected genomic DNA library" |
| cot selected genomic DNA library" |
| cot selected genomic DNA library |
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PUBFS60TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa045123,
genomic survey sequence.
BZ684738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Pantcoideae; Andropogoneae; Zea.

1 (bases 1 to 699)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick A., Frasest,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennetzen,J.
Unpublished
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  369 TCAGATGTAAATCCTTACATTTCACGCGCTTCATTCGCTGCTGGTCTCTATGGTGT 310
                                                                                376 GluGluLysLeuGluLeu---ProProProAlaSerGlyAsnValTyrAsn-----Asp 392
                                                                                                                                                                                  LysGluLeuProGlu---PheProAsnSerLeuGlnAsnAlaThrHisLeuLeuLysGlu 411
                                                                                                                                                                                                                            249 AAAGGACTAGTTGAAAGATTACCAAGATCATTAGCTGAATCAACTGAATTACTATCAAAA 190
                                                                                                                                                                                                                                                                                  SerLysMetLeuAsnLysThrPheGlyGluLysLeuIleLeuHisTyrValAsnAlaAla 431
                                                                                                                                                                                                                                                                                                            217 AlaAspProLeuThrMetAlaAspArgHisIleIleAlaLysHisGlyValArgGluMet
                                                                                                                               309 ATTAACAAATTAGAATTAAAACAAAAACCAATCATAGGTAATAGTTATGATCTCTATAAA
                                                                                                                                                                                                                                                                                                                                                                                  432 AsnValGluIleAsnGluPheSerLysGlnValThrAspTrpGluLeuAsnGln 449
                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: whitelaw@tigr.org
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Fax: 301-838-0208
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Best Local Similarity:
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AUTHORS
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DNA linear GSS 05-FEB-2003 genomic clone ZMMBTa029D11,
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1 (bases 1 to 818)
(Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Praser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTGGCAGCCGATCGTCGCCCGGAAATGGAGTTCTACCTG------ACC 140
  192 GCCGGGCGCCCGATCGAAGGCAACTCCTACGAGCAGATGGAG---CCGAGCCTGCCGAA 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. 818
| /organism="Zea mays" | / /organism="Zea mays" | / /organism="Zea mays" | / /organism="Zea mays" | / /organism="B7" | / /organism="Zea" | / /organism="Zea" | / /organism="Zea" | /organ
                                                                               135 CAACTTGCGCGACGCCTGCGCGAGCTGAACGCGAAATCATGGCGAAGTACATCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 ProLeuPheCysSerProArgVallleLeuMetGlnGlnIleGluArgLeuAlaAsnLeu
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                                                    nSerLeuGlnAsnAlaThrHisLeuLeuLysGluSerLysMetLeuAsnLysThrPheGl
                                                                                                                                                    120 yGluLysLeuIleLeuHisTyrValAsnAlaAlaAsnValGluIle 435
                                                                                                                                                                                                   cccgaagracarcarcarcarcarcaaggaaagcaaggra 30
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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PUBDI18TD ZM 0.6 1.0 KB Zea mays genomic survey sequence.
BZ687214 GI:28248163
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Class: sheared ends.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 AsnLeuLysThrAlaGlnProHisHisGlnTrpMetAsnIleSerAlaSerSerGlyIle
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                     /db_xref="taxon:287"
/clone="paces2-164 871"
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/note="clinical isolate 2-164 Whole genomic shotgun
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95
52
135
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| 936 GAGGTTGAAGTTTCCTACTTGAATCGGACTCAAGGGGCA----
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Matches:
Conservative:
Mismatches:
Indels:
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etrain="2-164"
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Mastigamoeba balamuthi
Bukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.

1 (Dases 1 to 1138)
Bapteste,E., Brinkmann,H., Lee,J.A., Moore,D.V., Sensen,C.W.,
Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and
Philippe,H.
The analysis of 100 genes supports the grouping of three highly
divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BEG36680 1138 bp mRNA linear EST 03-JAN-;
rockefeller.0.366 Mastigamoeba balamuthi lambda ZAP II Library
Mastigamoeba balamuthi cDNA similar to glutamine synthetase (EC
/dev_stage="Aggregation stage"
/clone lib="Dictyostelium discoideum cDNA library, AF"
| 109 c 108 g 256 t 9 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyraspGlnAsnaspGluTyrGlyMetSerThrLeuAlaArgAsnTrpIleAlaGlyLeu
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BJ358241 Dictyostelium discoideum cDNA library, AF Dictyostelium discoideum cDNA clone dda56b22 3', mRNA sequence.
BJ358241. GI:19257836
                                                                                                                                                                                                                                   440
     GAAACCGGTCGCCAGTCGTTTTCCATTGATGCGGCCAACGAATTCGACCCACTCTTCGAA 260
                                           SerValArgAsnLysLeuGluGluAlaGlyIleLeuMetGluAlaThrHisProGluPhe 205
                                                                               GACGICIACGACIGCIAGGCCCAGGCCTGGACCTCGACGTIGATCCACGAAGAC 320
                                                                                                                                                                                                                                                                         246 PheMetAlaLysLeuSerSerThrAlaLeuGlyAsnAlaCysHisIleHisMetSerLeu 265
                                                                                                                                                                                                                                                                                                                                                                                                                           ThrieuAlaArgAsnTrplleAlaGlyLeuLeuLysTyrValProGluAlaThrTyrPhe 305
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615 TITGCGCCCAACGTGAACTCGTTCCGTCCTGCCGGACACTTCGGCACCGGTCAAC 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             326 CysCysTrpAlaIleAspAsnArgThrSerAlaPheArgLeuCysAsnSerLysSerGlu 345
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Urushihara, T. Tanaka, Y., Kohara, Y. and Shin-i, T. Full length cDNA of Dictyostelium discoideum at the aggregation
                                                                                                                                                                                                                                                                                              206 LeuProSerGlnHisGluLeuAsnPheValProAlaAspProLeuThrMetAlaAspArg
                                                                                                                                                                                             HisllelleAlaLysHisGlyValArgGluMetAlaGluGlnSerGlyMetValAlaThr
                                                                                                                                                                                                                     501 GTCGACATCGCCACCGGCAAACCAGTGTTCGTCGACGACGTCGACGGC-----AACAAGAGT
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
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Dictyostelium discoideum

Dictyostelium discoideum

Bukaryota; Mycciozoa; Dictyosteliida; Dictyostelium.

1 (Dases 1 to 584)

Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M. Yoshino, R., Mitra, B. M., Pi, M., Sato, T., Takemoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.

The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
                                                                                                         380 GluLeuProProAlaSerGlyAsnVal-----TyrAsnAspLysGluLeuProGlu 397
                                                                                                                                          635 GACATCACCGACGTGCAGGACACGCGTATCGAGTACCGTGGAGGCGACGCGTCGGGCAGC
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Email: hideko@biol.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'
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Tel: 81-298-53-4664
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University of Tsukuba
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 Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
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Laboratory of Biochemical Parasitology
The Rockefeller University
130 York Avenue, New York, NY 10021, U
Email: mmuller@rockvax.rockefeller.edu
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(H.Urushihara)

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APPLICANT: IKEBA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAXOSHI
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APPLICANT: SHIBA, TADAXOSHI
APPLICANT: SHIBA, TADAXOSHI
APPLICANT: HATTORI MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 299-262
CURRENT APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 6703
LENGTH: 1362
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-Q=/Cgn2 1/USPTO spool/US10098602/runat 17122003 151240_28154/app_query.fasta_1.647
-D=-Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=6.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=blts -STRAT=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=200000000 -USER=1810109860.2 GCGN 1 1 353 @runat 17122003 151240_28154
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -KGAPOP=10 -XGAPEXT=0.5
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| Cgn2_6/ptodata/1/pubpna/US06_MW PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/US06_WW PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/US07_NEW PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/US08_WW PUB.seq:*
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| Cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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                          GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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422 LysLeulleLeuHisTyrValAsnAlaAlaAsnValGlulleAsnGluPheSerLysGln 441
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: BSHIKAWA, JUN
APPLICANT: HORIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: AATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR PLLICATION NUMBER: JP 2001-204089
PRIOR PLLING DATE: 2001-05-30
PRIOR PLLING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR PLING DATE: 2001-08-02
PRIOR PLING DATE: 2001-08-02
PRIOR PLING DATE: 2001-08-02
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142 GACGAGGTGCTGGAGGCACGGAGGATGCAACTACCTGCTCGCCGTCGACACCGAC
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   ORGANISM: Streptomyces avermitilis
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TITLE OF INVENTION: METHOD FOR PRODUCING L-GLUTAMINE BY FERMENTATION AND L-GLUTAMIN-
TITLE OF INVENTION: PRODUCING BACTERIUM
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                                                     LeuAlaPheSerAlaIleIleAlaAlaGlyIleSerGlyIleGluGluLysLeuGluLeu
                                                                                                     ProProProAlaSerGlyAsnValTyrAsnAspLysGluLeuProGluPheProAsnSer
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CURRENT APPLICATION NUMBER: US/10/062,458
CURRENT FILING DATE: 2002-02-05
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PRIOR FILING DATE: 2001-05-30
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PRIOR APPLICATION NUMBER: JP 2001-28163
PRIOR FILING DATE: 2001-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/10062458 Publication No. US20030003550A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IZUI, HIROSHI
MORIGUCHI, KAYO
KAWASHIMA, HIROKI
NAKAMATSU, TSUYOSHI
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SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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LOCATION: (2006)..(5200)
OTHER INFORMATION:
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LOCATION: (659)...
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8041832 CACCTGTCGCCGGACGCGGAC---GCCACCAACGCCATGGCCGACCGGACCCGGC 8041888
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                                                                                                                  AspMetGlnGlyArgLeuMetGlyLysArgLeuThrGlyArgHisPheLeuGlyLeuAsp
                                                AspGluLeuAsnAsnLeuIleArgAsnGlyLysIleAspThrValValLeuAlaCysVal
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              US-10-098-602A-2 (1-454) x US-10-156-761-1 (1-9025608)
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            390 TyrAsnAspLysGluLeuProGluPheProAsnSerLeuGlnAsnAlaThrHisLeuLeu
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PALENTIN NUMBER: JP 00/280988
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                            Sequence 2442, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
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ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NOOKO
SENOH, AKIHIRO
IKEDA, MASATO
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Best Local Similarity:
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US-09-738-626-2442
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                             ValTyrAlaValThrileGluGlyIleAlaGlyGlyGlyTyrGluIleSerSerValAsp
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                                                               -- CGTATCTCGGAAGCGGAC
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-----GAAGAAGGCATCGGATTCGAT
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GAAAAGTCAGAGCTTGTTGCTGACATCCTCGGTGAGCACGTTTTTGAGTTTT 8]aalaaanus16]utlaacnclubacartunclaus1mhraantnclut	GCGTGACTACCAAGAGCAG		US/09738626 .97605A1	IHS) POLYNUCLEOTIDES	US/09/738,626 12-18 : 99/377484	l6 9 00/159162 37 9 00/280988	93	jlutamicum	4.	Conservative Mismatches: Indels: Gaps:	US-09-738-626-1 (1-3309400	GIYLYSIIEABDINIYAINAINEUATACYSVAIASDMEUGINGIYAKGUER ::: ::: ::: GGCCACTTGAAGTCAGTGGTTGTGGCTCCTGCAGAACTAGAGTCTGCGTTC	sPheLeuGlyLeuAspGln ::	-GAAGAAGGCATCĠĠĀTTCĠĀĪ lThrileGluGlyileAlaGlyGly	GGCTCAGCCATTGAGGGCTACGCG	/8HisLeuCysAlaAspLeu ATTGCCCGCCCAGATCCA	AlaValLeuAlaIleSerAsnProHisAsnPheVal	ACTGCAGGCAGCACGCCTG
1207 GAAAAGTCAGAGCTTG		450 GlyPheAsn 452 ::: 1327 AATCTTGAT 1335	ion 0201	GENERAL INFORMATION: APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIXOGUCHI, HIROSHI APPLICANT: ANDO, SEIKO		SENOH, AKIHIRC IKEDA, MASATO OZAKI, AKIO NVENTION: NOVEL			PRIOR FILING DATE: 2000-08-03 NUMBER OF SEQ ID NOS: 7059 SOFTWARE: Patentin ver. 3.0 EQ ID NO 1	3309400 NAA M: Corynebacterium glutamicum 26-1		milarity: 47.08% Similarity: 28.94% h: 19.80%	02A-2 (1-454) x US-(35 ArgLeuThrGlyArgH				95 SerGluGlyAlava	
Db 12	1	Oy 4	RESULT 5 US-09-738-6 ; Sequence ; Publicati	GENERAL IN APPLICANT APPLICANT APPLICANT APPLICANT	; APPLICANT: ; APPLICANT: ; APPLICANT: ; APPLICANT:	; APPLICANT: ; APPLICANT: ; APPLICANT: ; TITLE OF I	; FILE RBF; CURRENT; CURRENT; PRIOR AF	PRIOR FI PRIOR AF PRIOR FI PRIOR FI	; PRIOR FIL. ; NUMBER OF ; SOFTWARE: ; SEQ ID NO	; LENGTH: 330 ; TYPE: DNA ; ORGANISM: C US-09-738-626-1	Alignment S Pred. No.: Score:	Percent Similarity Best Local Similar Query Match: DB:	US-10-098-602A-2	OY 15 Db 2364071	λō	Db 2364020 Qy 55	Db 2363999	Oy 75	ΛΌ	Db 2363912
 CTCCCACTA 243	110 ATGCCAGAC 303	ArgLeuAla 130 CTAGCTGCA 363	AsnGluThr 150	164 CCACCTGTG 447	ThrPheMet 184 AATTTCCGT 507	HisProglu 204 CACCATGAA 567	Metalaasp 224 ATGGCCGAC 627	MetValAla 244 ::: GTCGGGCA 687	HisMetSer 264 	TyrGlyMet 284 ::: TACATGCTG 801	AlaThrTyr 304 TTCACCGCT 861	AlaProThr 324 GCTCCAACT 921	, ,	AshProTyr 361	AACCCATAT 1041	LeuGluLeu 381 TATGAGCTC 1101		GCCATGGGC 1161 HisLeuLeu 409	::: CGCCAAATG 1206	TyrValAsn 429 ::::::
-ATTGCCCGCCCAGATCCATCGACATTCCAGGTCCTCCCACT	SerGluGlyAlaValLeuAlalleSerAsnProHisAsnPheValThr	SerGluProLeuPheCysSerProArgVallleLeuMetGlnGln1leGluArgLeuAl 	AsnLeuLysLeuLysGlyLeuPheAlaSerGluLeuGluPheAsnLeuPheAsnGluTh :::	TyrLysSerAlaSerGlnLysHisTrpLysAsnLeuLysThr	AlaGlnProHisHisGlnTrpMetAsnIleSerAlaSerSerGlyIleGluThrPheMeii: :: ::	ArgSerValArgAsnLysLeuGluGluAlaGlyIleLeuMetGluAlaThrHisProGl :: GAAACGCGATGGTAGCGCTGGAGGAACTCGGCATCCCTGTCGAGTTCTCCCACCATGA	205 PheLeuProSerGlnHisGluLeuAsnPheValProAlaAspProLeuThrMetAlaAs 	ArgHisIleIleAlaLysHisGlyValArgGluMetAlaGluGlnSerGlyMetValAl 	ThrPheMetalaLysLeuSerSerThralaLeuGlyasnalaCysHisIleHisMetSe 	265 LeuGlnAspAlaGluThrGluLysAsnAlaPheTyrAspGlnAsnAspGluTyrGlyMe 	SerThrLeuAlaArgAsnTrpIleAlaGlyLeuLeuLysTyrValProGluAlaThrTy 	305 PhePheAlaSerTyrIleAsnSerTyrLysArgLeuGlnProLeuThrPheAlaProTh 	LysCysCysTrpAlaIleAspAsnArgThrSerAlaPheArgLeuCysAsn LysCysCysTrpAlaIleAspAsnArgThrSerAlaPheArgLeuCysAsn	342 SerLygSerGluGlyIleAsnValGluLeuArglleGlyGlyAlaAspLeuAsnProTy	:::: GTCTTCCTGATACCGCTTGT	LeuAlaPheSerAlaIleIleAlaAlaGlyIleSerGlyIleGluGluLysLeuGluLe TTGGCGTTTTCAGTGATGCTCGGCGCTGGTTTGAAAGGCATTAAAGAAGGTTATGAGCT	ProProProAlaSerGlyAsnVal	TGAGCTTCCGGGAACGTCGC SnSerbeuGlnAsnAlaThr	 TACAACGATCTGCCAAGCAGCCTTGATCAGGCACTGCCCAAAT	410 LysGluSerLysMetLeuAsnLysThrPheGlyGluLysLeuIleLeuHisTyrValAs
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199 ACC	95 SerGluGly 244 GAAGCGGGCATC	111 SerGluProLeuricker	131 AsnLeuLysLeu 	151 TyrLysSerAle	165 AlaGlnProHie ::: 448 CCCACTGACAAC	185 ArgSerValArg :: 508 CGAACGCGATC	205 PheLeuProSe: 568 ACTGCACCTGGC	225 ArgHisIlelle ::: 628 AACATCATGACC	245 ThrPheMetals::: 688 TCATTTATGCCC	265 LeuGlnAspAld ::: 748 TTATTGAGGG	285 SerThrLeuAle	305 PhePheAlaSe1 862 GTGACCAACCAC	325 LysCysCysTrr	342 SerLysSerGlu	982 AATAAGGAGGA(362 LeuAlaPheser 	382 ProProProAle	110z GACGAGCCAGCT	 1162 TACAACGAT	410 LysGluSerLy: ::::: :::
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                        FILE REFERENCE: 2074/100
CURRENT APPLICATION NUMBER: US/09/733,383
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 09/155,183
PRIOR FILING DATE: 1997-03-24
                                                                                           Sequence 12, Application US/09733383
Patent No. US20010014467A1
GENERAL INFORMATION:
APPLICANT: Narbad, Arjan
                                                                                                                                APPLICANT: Rhodes, Michael J.C., APPLICANT: Gasson, Michael J. APPLICANT: Walton, Nicholas J. TITLE OF INVENTION: PRODUCTION:
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Matches:
     FILING DATE: 1998-09-22
APPLICATION NUMBER: 09/733,383
FILING DATE: 2000-12-07
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 4259
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GluLeuAsnPheValProAlaAspProLeuThrMetAlaAspArgHisIleIleAlaLys
                                                                                      LeuGluGluAlaGlyIleLeuMetGluAlaThrHisProGluPheLeuProSerGlnHis
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APPLICANT: Rades, Michael John
APPLICANT: Gaseon, Michael John
APPLICANT: Walton, Michael John
TITLE OF INVENTION: PRODUCTION OF p-HYDROXYBENZOIC ACID
FILE REFERENCE: 20747/103
CURRENT APPLICATION NUMBER: 18/10/199,405
CURRENT FILING DATE: 2002-07-17
PRIOR PILING DATE: 2002-07-17
PRIOR PLILING DATE: 1996-03-23
PRIOR FILING DATE: 1997-03-24
PRIOR FILING DATE: 1997-03-24
PRIOR PLILING DATE: 1997-03-24
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Publication No. US20030167511A1
GENERAL INFORMATION:
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166 TCTTCTATTGAAGGTTTT--------
SOFTWARE: FastSEQ for Windows Version
                                                               TYPE: DNA ORGANISM: Streptococcus pneumoniae
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                                            1170 ATGACCGGCGAGCCTGGCAGCGCCATGCACCTGCACCAGAGCATCATCGATATCGAGACC 1229
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APPLICANT: Trail, John D.
APPLICANT: Trail, John D.
APPLICANT: Trail, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 60/201,078
PRIOR APPLICATION NUMBER: 60/201,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
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PRIOR FILING DATE: 2000-10-23
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PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
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PRIOR PILING DATE: 2000-11-27
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Patent No. US20020061569A1
GENERAL INFORMATION:
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APPLICATION WUMBER: 60/269,308
FILING DATE: 2011-02-16
R OF SEQ ID NOS: 14110
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Zyskind, Judith W.
Wall, Daniel
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                                                                                                                               TrplleAlaGlyLeuLeuLysTyrValProGluAlaThrTyrPhePheAlaSerTyrIle 310
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AsnAlaPheTyrAspGlnAsnAspGluTyrGlyMet----SerThrLeuAlaArgAsn
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HARIKAWA, HINGHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
FRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
FRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5911, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Streptomyces avermitilis
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; NAME/KEY: CDS
; LOCATION: (1)..
US-10-156-761-5931
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293 AlaGlyLeuLeuLysTyrValProGluAlaThrTyrPhePheAlaSerTyrIleAsnSer 312
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                                                                                                                                       22 LeualaCysValaspMetGlnGlyArgLeuMetGlyLysArgLeuThrGlyArgHisPhe 41
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                                             ThrileThrTyrAspGluLeuAsnAsnLeuIleArgAsnGlyLysIleAspThrValVal
                                                                                           13 ACTITCACTARAGACGACATTCGTARATTTGCAGAAGGAAAATGTAAGATATTTAAGA
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US-10-098-602A-2 (1-454) x US-09-815-242-4678 (1-1338)
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                          354 GlyGlyAlaAspLeuAsnProTyrLeuAlaPheSerAlaIleIleAlaAlaGlyIleSer 373
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APPLICANT: 401. Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: 1601.61-61-61
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-22-6
PRIOR FILING DATE: 2001-22-6
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PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-21
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Matches:
Conservative:
Mismatches:
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Patent No. US20020061569A1
GENERAL INFORMATION:
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Zyskind, Judith W.
Wall, Daniel
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith V
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Best Local Similari
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LENGTH: 1338
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Match: 17.87% Indels: 9 Gaps:	OS-10-098-802A-2 (1-454) x OS-09-815-242-8240 (1-1341) QY 2 ThrileThrTyrAspGluLeuAsnAsnLeuileArgAsnGlyLysileAspThrValVal 21	Qy 22 LeualaCysValaspMetGlnGlyArgLeuMetGlyLysArgLeuThrGlyArgHisPhe 41	Qy 42 LeuGlyLeuAspGlnLysLysIleSerIleSerThrPheValTyrAlaValThrIleGlu 61 :::	Oy 62 GlyllealaGlyGlyTyrGluIleSerSerValAspThrGlyTyrSerAspCysHis 81	Oy 82 LeuCysAlaAspLeuAsnSerLeuHisLeuLeuProTrpSerGluGlyAlaVal 99	Qy 100 LeualaileSerasnProHisasnPheValThrSerGluProLeuPheCysSerProArg 119	Qy 120 ValileLeuMetGlnGlnileGluArgLeuAlaAsnLeuLysLeuLysGlyLeuPhe 138 :: ::: :: Bb 334 GCAAACTTAAAAGGAAATGGAAGATTTAGGCTTCACAGACTTTAACCTA 393	Qy 139 AlaSerGluLeuGluPheAsnLeuPheAsnGluThrTyrLysSerAlaSerGlnLysHis 158	Oy 159 TrpLysAsnLeuLysThrAlaGlnProHisHisGlnTrpMet 172	Qy 173 AsnIleSerAlaSerSerGlyIleGluThrPheMetArgSerValArgAsnLysLeuGlu 192	Oy 193 GlualaGlyIleLeuMetGlualaThrHisProGluPheLeuProSerGlnHisGluLeu 212	Qy 213 AsnPheValProAlaAspProLeuThrMetAlaAspArgHisIleIleAlaLysHisGly 232	Qy 233 ValargGluMetAlaGluGlnSerGlyMetValAlaThrPheMetAlaLygLeuSerSer 252	Oy 253 ThrAlaLeuGlyAsnAlaCysHisIleHisMetSerLeuGlnAspAlaGluThrGluLys 272	Oy 273 ASNAlaPheTyrAspGlnAsnAspGluTyrGlyMetSerThrLeuAlaArgAsnTrplle 292	Oy 293 AlaGlyLeuLeuLysTyrValProGluAlaThrTyrPhePheAlaSerTyrIleAsnSer 312	Oy 313 TyrLysArgLeuGlnProLeuThrPheAlaProThrLysCysCysTrpAlaIleAspAsn 332
Qy 353 IleGlyGlyAlaAspLeuAsnProTyrLeuAlaPheSerAlaIleIleAlaAlaGlyIle 372 Db 1012 TCAGTAGATCCAGATGCCATAAGATGCTGTAAAGATGTTAAAGATGTTAAAAGATGATGAAAGATGTTAAAAGATTAAAGATGAAAGATTAAAAGATGAAAGATTAAAAGATGAAAGATTAAAAGATGAAAGATTAAAAAGATGAAAAGATTAAAAAGATGAAAAGATTAAAAAGATGAAAAGATTAAAAAA	373 SerGly1leGluGluLy8LeuGluLeuProProProAlaSerGlyAsnValTy 1072 GATGGTATTAAAATTAAAAGTTCCAGAACCAGTTAACAAAATTTA	Qy 391 AsnaspLysGlu	Qy 406 ThrHisLeuLeuLysGluSerLysMetLeuAsnLysThrPheGlyGluLysLeulleLeu 425	Qy 426 HisTyrValAsnalaAsnValGluIleAsnGluPheSerLysGlnValThrAspTrp 445 1252 CAATTATTAATTCAAAATCAATTGAATGGGATTACTACAGAACTCAAGTATCTGAATGG 1311	Qy 446 GlubeuAsnGlnGlyPheAsnArgTyr 454 Db 1312 GAAAGAGATGATGAGCAATAT 1338	NESULT 11 US-09-815-242-8240 ; Sequence 8240, Application US/09815242	FACENCE NO. DESCORPTION: APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.		; APPLICANT: Tammamoco, Kobert T. ; TITLE OF INVENTION: Identification of Essential Genes in ; TITLE OF INVENTION: Prokaryotes	KEFEKENCE: EL NT APPLICATION NT FILING DATE APPLICATION N				FAIDTR FILTEN DATE: 2001-02-15; NUMBER OF SEQ ID NOS: 14110; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 8240; TANDARE: 1341	-i a		Alignment Scores: Alignment Scores: Score: 42.50 Autches: Percent Similarity: 45.84* Conservative: Best Local Similarity: 26.23* Mismatches: 21

Score: 424.50 Matches: 123 Percent Similarity: 45.84\$ Conservative: 92 Best Local Similarity: 26.23\$ Mismatches: 211 Query Match: 17.87\$ Indels: 43 DB: 9 US-10-098-602A-2 (1-454) x US-09-815-242-8677 (1-1341)	Qy 2 ThrileThrTyrAspGluLeuAsnAsnLeuileArgAsnGlyLysileAspThrValVal 21	Qy 22 LeualaCysValAspMetGlnGlyArgLeuMetGlyLysArgLeuThrGlyArgHisPhe 41	Oy 42 LeuGlyLeuAspGlnLysLysIleSerIleSerThrPheValTyrAlaValThrIleGlu 61 :::	Qy 62 GlylleAlaGlyGlyTyrGluIleSerSerValAspThrGlyTyrSerAspCy9His 81	Oy 82 LeuCy8AlaAspLeuAsnSerLeuHisLeuLeuProTrpSerGluGlyAlaVal 99	Qy 100 LeualaIleSerAsnProHisAsnPheValThrSerGluProLeuPheCysSerProArg 119	120 ValileLeuMetGlnGlnIleGluArgLeuAlaAsnLeuLy8LeuLy8GlyLeuPhe	Db 334 GCARAACTTRARAACGTGTATTRARAAGAAATGGAAGATTTAGGCTTCACAGACTTTAACCTA 393 Qy 139 AlaSerGluLeuGluPheAenLeuPheAsnGluTrTyrLysCyrAlaSerAlaSerGlnLysHis 158	394	Oy 159 TrpLysAsnLeuLysThrAlaGlnProHisHisGlnTrpMet 172 :: ::	Qy 173 ABnIleSerAlaSerSerGlyIleGluThrPheMetArgSerValArgABnLyBLeuGlu 192	Oy 193 GlualaGlyIleLeuMetGlualaThrHisProGluPheLeuProSerGlnHisGluLeu 212 :::	213 AsnPheValProAlaAspProLeuThrMetAlaAspArgHisIleIleAlaLysHisGly	Db 598 GACITIAAATAIGCAGAIGCTGTIACAGCAIGIGAIAAIATCCAAACAITIAAATIGGIT 657 Ov 233 ValaroglumetalaglugluSerglvmetValalaIhrphemetalaLvsbeuserSer 252	658 GITAAAACAAICGCACGTAAACATAATTACACGCAACAITTATGCCTAAACCAITATTC	Qy253 ThrAlaLeuGlyAsnAlaCysHisIleHisMetSerLeuGlnAspAlaGluThrGluLys 272	273 AgnAlaPheTyrAspGlnAsnAspGluTyrGlyMetSerThrLeuAlaArgAsnTrpIle	Db 772 AATGCATTCTTTGATCCAAATACTGAAATGGGCTTAACGGAAACTGCATATCAAATGCGTTAACGGAAACTGCATATTACA 831	293 AlaGlyLeuLeuLysTyrValProGluAlaThrTyrPhePheAlaSerTyrIleAsnSer 3	Db 832 GCAGGTGTGCTTAAAAATGCACGCGGATTTACTGCTGTATGTA
<pre>Qy 333 ArgThrSerAlaPheArgLeuCysAsnSerLysSerGluGlylleAsnValGluLeuArg 352</pre>	Qy 373 SerGly1leGluGluLysLeuGluLeuProProProAlaSerGlyAsnValTyr 390	Qy 391 AsnAspLysGluLeuProGluPheProAsnSerLeuGlnAsnAla 405	Oy 406 ThrHisLeuLeuLysGluSerLysMetLeuAsnLysThrPheGlyGluLysLeuIleLeu 425	Qy 426 HisTyrValAsnalaalaAsnValGluIleAsnGluPheSerLysGlnValThrAspTrp 445 ::::	Qy 446 GlubeuasnGlnGlyPheasnargTyr 454	RESULT 12 US-09-815-242-8677 ; Sequence 8677, Application US/09815242	; Patent No. US20020061569A1 ; GENERAL INFORMATION: ; APPLICANT: Haselbeck, Robert	; APPLICANT: Ohleen, Kari L. ; APPLICANT: Zyekind, Judith W. ; APPLICANT: Wall, Daniel	; APPLICANT: Trawick, John D. ; APPLICANT: Carr, Grant U	<pre>// AFFLICANT: Amendon, Robert 1. / APPLICANT: Xu, H. Howard // TITLE OF INVENTION: Identification of Essential Genes in / TITLE OF INVENTION: Prokaryotes</pre>	; FILE REFERENCE: ELITRA.011A ; CURRENT APPLICATION NUMBER: US/09/815,242 ; CURRENT FILING DATE: 2001-03-21 ; PRIOR APPLICATION NUMBER: 60/191,078		FILING DATE: 2000-09 APPLICATION NUMBER: FILING DATE: 2000-10	; PRIOR APPLICATION NUMBER: 60/253,625 ; PRIOR FILING DATE: 2000-11-27 : PRIOR APPLICATION NUMBER: 60/257,931	FILING DATE: 2000-12 APPLICATION NUMBER:	; PRION FILING DATE: 2011-02-16; NUMBER OF SEQ ID NOS: 14110; SOFTWARE: FastSEQ for Windows Version 4.0; SPC ID NO 8677	; LENGTH: 1341 ; TYPE: DNA	; ORGANISM: Staphylococcus aureus ; FEATURE:	; NAMEKKEY: CDS ; LOCATION: (1)(1341) US-09-815-242-8677	Alignment Scores: 2.62e-44 Length: 1341

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Percent Similarity:
Best Local Similarity:
                  Alignment Scores:
Pred. No.:
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1132 AACCGTGAAGAAGGTGAAGGGAGTAGGGATTCAAGACTTACCTTCAACACTTTATACTGCA 1191
                                                                                                                                                                                   406 ThrHisLeuLeuLysGluSerLysMetLeuAsnLysThrPheGlyGluLysLeuIleLeu 425
                                                                                                                                                                                                                                                                                                                 1192 TTAAAAGCAATGCGTGAAATGAAGTTATTAAAAAGCTTTAGGAAATCATATCTATAAT 1251
                                                                                                      353 IleGlyGlyAlaAspLeuAsnProTyrLeuAlaPheSerAlaIleIleAlaAlaGlyIle 372
                                                                                                                                                                 SerGly11eGluGluLysLeuGluLeuProProProAlaSerGlyAsnValTyr---- 390
                                                                                                                                                                                                                           AsnAspLysGlu------LeuProGluPheProAsnSerLeuGlnAsnAla 405
ArgThrSerAlaPheArgLeuCysAsnSerLysSerGluGlyIleAsnValGluLeuArg
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APPLICANT: Tawick, John D.
APPLICANT: Sarat J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: X. H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REPERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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PRIOR FILING DATE: 2000-03-21
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PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-16
PRIOR SEQ ID NOS: 14110
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                                                                                                                                                                                                                                                                                                                                                                                                          GluLeuAsnGlnGlyPheAsnArgTyr 454
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Patent No. US20020061569A1
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Zyskind, Judith W.
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APPLICANT: Zyskind, Jud:
APPLICANT: Wall, Daniel
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NAME/KEY: CDS

LOCATION: (1)...(1356)

US-09-815-242-6417
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Indels:
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     Length:
Matches:
2.26e-41
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44.81%
28.86%
16.92%
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DB: 10 Gaps: 7	US-10-098-602A-2 (1-454) x US-09-070-927A-188 (1-4176)	Qy 78 SerAspCysHisLeuCysAlaAspLeuAsnSerLeuHisLeuLeuProTrpSerGluGly 97	Db 308 AGTGACATGTATTTATACCCTGACCTATCTACATGGATGATTTTTCCGTGGAAAGCGAC 367	Qy 98AlaValLeuAlaIleSerAsnProHisAsnPheValThrSer 111		Oy 112 GluProLeuPheCysSerProArgvalIleLeuWetGlnGlnIleGluArgLeuAlaAsn 131 Db 416 ACCCTTTTGCCGGAGATCCCCG	132 LeulysLeuLysGlyLeuPheAlaSerGluLeuGluPheAsnLeuPheAsn		Oy 149GluThrTyrLy8SerAlaSerGlnLy8Hi8TrpLy8AenLeuLy8ThrAlaGln 166	Db 506 GAACCAGAATTTTTCCTATTTAAATTAGATGAGAATGGTGAAATTACCACTGACTTGAAT 565	ProHisHisGlnTrpMetAsnIleSeralaSerSerGlyIleGluThrPheMetArgSer	GATAAAGGTGGCTATTTTGATTTTGCACCAACCGATTTAGGTGAAAATTGTCGCCGTGAT	187 ValArgAsnLysLeuGludluAlaGlyIleLeuMetGluAlaThrHisProGluPheLeu 20		207 ProSerGlnHisGluLeuAsnPheValProAlaAspProLeuThrMetAlaAspArgHis 22	Db 686 CCTGGTCAACATGAAATTGACTTTAAATATGCTGATGTAGTTGATGCTTGTGACAATATT 745	Qy 227 IleIleAlaLyBHisGlyValArgGluMetAlaGluGlnSerGlyMetValAlaThrPhe 246	Db 746 CAAACGIICAAAITAGIIGIGAAAACTAIIGCGCGIAAACAIGGTIGCAIGCAACAITT 805	Qy 247 MetAlaLysLeuSerSerThrAlaLeuGlyAsnAlaCysHisIleHisMetSerLeuGln 266	Db 806 ATGCCAAAACCTTTGTTTGGAATTAATGGTTCTGGTATGCACTGCAATATGTCATTA 862	Qy 267 AspAlaGluThrGluLy9AsnAlaPheTyrAspGlnAsnAspGluTyrGlyMetSerThr 286	202 100.0 1 Proclamment of location in the land of the	920 ACTGCGTATCATTACTTAGGTGGTTTATTAAAAACATGCCCGTGCCTATACTGCGGTATGT	Qy 307 AlaSerTyrIleAsnSerTyrLysArgLeuGlnProLeuThrPheAlaProThrLysCys 326	Db 980 AACCCAACAGTGAACTCTTATAAACGCTTGGTACCAGGTTATGAAGCACTGTTTATGTA 1039	Qy 327 CysTrpAlalleAspAsnArgThrSerAlaPheArgLeuCysAsnSerLysSerGluGly 346	Db 1040 GCTTGGAGCGGCAGAAATCGTTCACCACTCATTCGAGTTCCTGAATCTCGTGGKTTATCG 1099	Qy 347 IleAsnValGluLeuArgIleGlyGlyAlaAspLeuAsproTyrLeuAlaPheSerAla 366	Db 1100 ACTCGTTTAGAATTACGTTCTGTCGATCCTTCAGCGAATCCGTATTTAACAATGGCTGTC 1159	Oy 367 IlelleAlaAlaGlyIleSerGlyIleGluGluLysLeuGluLeuProProAlaSer 386	Db 1160 TTATTACAAGCATTTGGATGGTATTCGTAATGAACTTACACCACCGCCAGCAGTTGAT 1219	Qy 387 GlyAsnValTyrAsnAspLysGluLeuProGluPhePro 399		Qy 400 AsnSerLeuGlnAsnAlaThrHisLeuLeuLysGluSerLysMetLeuAsnLysThrPhe 419
Db 1069 TTATTACAAGCTGGTTTGGATGGTATTCGTAATGAACTTACGCCACCGCCAGCAGTTGAT 1128	387 GlyAsnValTyrAsnAspLysGluLeuProGlu	Db 1129 CGTAATATTTATGTGATGAATGAGGAAGAACGTCAACATGCACAAATTGAAGATTTGCCA 1188	Qy 400 AsnSerLeuGlnAsnAlaThrHisLeuLysGluSerLysMetLeuAsnLysThrPhe 419	Db 1189 TCAACCTTACACAATGCCATCAAAGAATACGTAAAGATCAAGTAATGATTGAT	Qy 420 GlyGluLysLeuIleLeuHisTyrValAsnAlaAsnValGluIleAsnGluPheSer 439	Db 1249 GGTCGTCATATTTTGCCAATTTTGTAGAAGGAAACGAATGGAATGGGCAGCCTTCCGT 1308 Ov 440 IvsglnValThrashTroGlnienasaGlnGlnGlvPheasnArdTvr 454	1309 CAAACCGTTTCTGAATGGGAAAGAGAAAATATTTGGAGTTGTAC	RESULT 14	US-09-070-927A-188 ; Sequence 188, Application US/09070927A ; Datest No reconcontained	GENERAL INFORMATION:	Patrick J. Steven Bara	; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides ; NUMBER OF SEQUENCES: 982	CORRESPONDENCE ADDRESS:	; STREET: 9410 Key West Avenue ; CITY: Rockville	STATE: Maryland	; ZIP: 20850 ; COMPUTER READABLE FORM:	MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage; COMPUTER: HP Vectra 486/33	OPERATING SYSTEM: MSDOS version 6.2	CURRENT APPLICATION DATA:	; FILING DATE: 04-May-2000 : CLASSIFICATION: <unknown></unknown>	PRIOR APPLICATION DATA: APPLICATION UNBER: 60/046,655 DITING DATE: 1007-06-16		CALLING DATE: 1997-11-14 FILING DATE: 1997-11-14	ATTORNEY/AGENT INFORMATION: NAME: Kenley K. Hoover DESTRUCTION MINISTED A 200	REGISTATION NOTION: 10,302 REFERENCE/DOCKET NUMBER: PB369	3: (30)	; INFORMATION FOR SEQ ID NO: 188:	SEQUENCE CHARACTERISTICS: LENGTH: 4176 base pairs	STRANDEDNESS double	; SEQUENCE DESCRIPTION: SEQ ID NO: 188: US-09-070-927A-188	03-03-03-03-03-03-03-03-03-03-03-03-03-0	1.57e-40 Length: 402.00 Matches:	t Similarity: 44.81% ocal Similarity: 28.86%	16.92% Indels:

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945 GAATGGGATATGTTCCGCACACAGTCCATCCTTGGGAGCGCGAGCAGTATATGTCTCAG 1004
    321 PheAlaProThrLysCysCysTrpAlaIleAspAsnArgThrSerAlaPheArgLeuCys 340
                                                                                                                                                                                 TyrLeuAlaPheSerAlaIleIleAlaAlaGlyIleSerGlyIleGluGluLysLeuGlu 380
                                                                                                                                                                                                                                                                       381 LeuProProProAlaSerGlyAsnValTyr-------AsnAspLys 393
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                                                                                                                                                                                                           394 GluLeuProGluPheProAsnSerLeuGlnAsnAlaThrHisLeuLeuLysGluSerLys
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                                                                                            341 AsnSerLysSerGluGlyIleAsnValGluLeuArgIleGlyGlyAlaAspLeuAsnPro
                                                                                                                     645 GCTTCCCGCGGCATCAGCACGCGCTAGAAGTCAGAAGCGTAGACCCTTCTGCGAACCG
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Job time : 19019 secs
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                                                                                                                                                                                    440 LysGlnValThrAspTrpGluLeuAsnGlnGlyPheAsnArgTyr 454
                                                                                                                                                                                                                                                                                Sequence 261, Application US/09974300
| Patent No. US20020146721A1
| GENEBAL INPORMATION:
| APPLICANT: Clausen, Ib Groth
| TITLE OF INVENTION: Methods For Monitoring Multiple Gene
| TITLE OF INVENTION: Expression
| FILE REFERENCE: 10085.500-US
| CURRENT APPLICATION NUMBER: US/09/974,300
| FRICR PAPLICATION NUMBER: 09/680,598
| PRIOR FILING DATE: 2001-10-06
| PRIOR FILING DATE: 2000-10-06
| PRIOR FILING DATE: 2000-13-06
| PRIOR FILING DATE: 2001-03-27
| PRIOR FILING DATE: 2001-03-27
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Sequence 151, App
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Sequence 10, Appl
Sequence 10119, A
Sequence 225, App
Sequence 225, App
Sequence 225, App
Sequence 2431, Ap
Sequence 2433, Ap
Sequence 11761, App
Sequence 1177, App
Sequence 1177, App
Sequence 11176, App
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Sequence 1, Appli
Sequence 2330, Ap
Sequence 2389, Ap
Sequence 216, App
Sequence 216, App
Sequence 16240, A
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Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: PRASER, Claire M.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOPTHARE: PATENTIN VOY: 2.1
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US-09-134-01154
US-08-916-4218-1
US-09-252-991A-10119
US-09-252-991A-1251
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-09-252-991A-208
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Best Local Similarity:
    LENGTH: 4403765
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US-09-103-840A-2/c
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-MODEL=frame+_p2n.model -DEV=xlh
-Q=/CQm1_1/USPTO spool/USI0086602/runat_17122003_151238_28076/app_guery.fasta_1.647
-Q=/CQm2_1/USPTO spool/USI0086602/runat_17122003_151238_28076/app_guery.fasta_1.647
-DB=ISGUEG_PATEPTO STRATE=1 -SNDE-1.MATRIX=DIGBUEG_2 -TRANS=human40.cdi
-LOOPEXT=0 -UNITS=51Es -START=1 -SNDE-1.MATRIX=DIGBUEG_2 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODEL-LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MININEN=0 -MAXLEN=200000000
-USRR=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MININEN=0 -MAXLEN=200000000
-USRR=US10098602_@CGN 1_1.56 @VUNAt 1/122003_151238_28076_NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DBV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAROP=10 -XGAREXT=0.5 -FGAROP=6
-FGAREXT=7 -YGAROP=10 -YGARDEXT=0.5 -DBLOP=6 -DBLEXT=7
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Sequence 1330, Ap
Sequence 1310, Ap
Sequence 1279, Ap
Sequence 10926, A
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Sequence 10987, A
                                                                                                                                             December 17, 2003, 22:53:00 ; Search time 299 Seconds (without alignments) 670.194 Million cell updates/sec
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   /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
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- 2003 Compugen Ltd.
                                                                                                    - nucleic search, using frame_plus_p2n model
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US-09-252-991A-1285
US-09-252-991A-1299
US-09-252-991A-10926
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US-09-103-840A-1
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Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
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3165847 TTCGGCGAGGAGGATGTTGTCGCCACTACCTGAACACGCGCGTGTGGAGCTGGCGCGTTC 3165788
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                                                                                  CTTCAGCTGCCCGAGCCCTGTGTGCGCAACGCCTACCAAGGCGCCGATGTCGAACGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 IleThrTyrAspGluLeuAsnAsnLeuIleArgAsnGlyLysIleAspThrValValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AlaCysValAspMetGlnGlyArgLeuMetGlyLysArgLeuThrGlyArgHisPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gly11eAlaGlyGlyGlyTyrGluIleSerSerValAspThrGlyTyrSerAspCysHis
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                                                             LeuGluLeuProProAlaSerGlyAsnValTyrAsnAspLysGluLeuProGluPhe
                                                                                                                                             ProAsnSerLeuGlnAsnAlaThrHisLeuLeuLysGluSerLysMetLeuAsnLysThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --- GlyLeuAspGlnLysLysIleSerIleSerThrPheValTyrAlaValThrIleGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-23001.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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Matches:
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ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
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; Sequence 1, Application US/09103840A
; Patent No. 6294328
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                               3167086 TIGGCGTGGACCGAGTTGGAGCGACTGGTCGCGGCGGCGGTGACGTCGACGTCGACGTCACCGTCACGTC 3167027
                                                                                                       3167026 GCGTTCACCGACATGCAGGCCGGCTGGCCGGCAAACGGATATCGGCCGCATTTCGTC 3166967
                                                                                                                                                                                            3166966 GACGACACCCCCCCCCCGCGTGCTGCTGCTGTATCTGCTGCCCTGGACGTCGAC 3166907
                                                                                                                                                                                                                                                                                                                                                      3166846 ATGACGCCGGACTTGTCCACTCTGCGCTGATTCCTTGGCTACCGGGAACGCCCTGGTG 3166787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3166321 TGTCACATGTCTCGCTGCGTGGCACGGATGCCTCCGCG---GTGTTTGCCGACAGT 3166265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3166264 AACGGGCCGCACGCATGTCGTCGATGTTCCGCAGCTTCGTCGCCGGCCAGTTGGCCACG 3166205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3166204 TIGGGGGAATTGACGCTGTGCTATGCGCCGACCATTAACTCCTACAAGGGATTTGCCGAT 3166145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3166144 AGCAGTTTCGCGCCGACGCCTTGGGGCCTGGACCATCGCACCTGCGCCTGCGG 3166085
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APPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 1330

LENGTH: 1350
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Sequence 1330, Application US/09252991A
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APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR PILING DATE: 1999-02-18

PRIOR PLILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

ENGOTH: 2538
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                              2214 GGCTGGCAACCGGTGGTGGCCACCGAACTGGAGTTCTTCGTCTTTCGCCCCGGAACACCGAT 2155
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Patent No. 6551795
GENERAL INFORMATION:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
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; Sequence 1279, Application US/09252991A
; Patent No. 6551795
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ORGANISM: Pseudomonas aeruginosa
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT FILING DATE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR PPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR PILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-02-18 NUMBER OF SEQ ID NOS: 33142 SEQ ID NOS: 33142 SEQ ID NOS: 33142
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                                                                                                                                                                                                                                              406 ThrHisLeuLeuLysGluSerLysMetLeuAsnLysThrPheGlyGluLysLeuIleLeu
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Best Local Similarity:
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                    364 GGTGATCCCTTCTTCGCCGACCCCCGCGAAGTCCTGCGCCAGGTGGTGGCCAGGTTCACC 423
                                                                                                                              ThrTyrLysSerAlaSerGlnLysHisTrpLysAsnLeuLysThrAlaGlnProHisHis 169
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Sequence 1417, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196, 136
CURRENT PALLING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PAPLICATION NUMBER: US 60/074,788
PRIOR PAPLICATION NUMBER: US 60/094,190
PRIOR PLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 1417
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Matches:
Conservative:
Mismatches:
Indels:
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452.00
47.58%
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Best Local Similarity:
US-09-252-991A-11417/c
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milarity: 28.38\$ Mismatches:	18.94% Indels:	US-10-098-602A-2 (1-454) x US-09-252-991A-11262 (1-1470)	Qy 1 MetThr1leThrTyrAspGluLeuAsnAsnLeu1leArgAsnGlyLys1leAspThrVal 20	Oy 21 ValleuAlaCysValAspMetGlnGlyArgLeuMetGlyLysArgLeuThrGlyArgHis 40	Oy 41 PheLeuGlyLeuAspGlnLysLysIleSerIleSerThrPheValTyrAlaValThrIle 60	Qy 61 GluGlyIleAlaGlyGlyGlyTyrGluIleSerSerValAspThrGlyTyrSerAspCys 80	Qy 81 HisLeuCysAlaAspLeuAsnSerLeuHisLeuLeuProTrpSerGluGlyAlaVal 99	Qy 100 LeuAlaIleSerAsnProHisAsnPheValThrSerGluDroLeuPheCysSerProArg 119	Qy 120 VallleLeuMetGlnGlnIleGluArgLeuAlaAsnLeuLysLeuLysGlyLeuPheAla 139	Qy 140 SerGluLeuGluPheAsnLeuPheAsnGluThr	Qy 151TyrLysSerAlaSerGlnLysHisTrpLysAsnLeuLysThrAlaGlnPrOHis 168	Qy 169 HisGlnTrpMetAsnIleSerAlaSerSerGlylleGluThrPheMetArgSerValArg 188	Qy 189 AsnLysLeuGluGluAlaGlylleLeuMetGluAlaThrHisProGluPheLeuProSer 208	Oy 209 GlnHisGluLeuAsnPheValProAlaAspProLeuThrMetAlaAspArgHisIleIle 228	Qy 229 AlaLysHisGlyValArgGluMetAlaGluGlnSerGlyMetValAlaThrPheMetAla 248	249 LysLeuSerSerThrAlaLeuGlyAsnAlaCysHisIleHisMetSerLeuGlnAspAla 26	DD 859 AAGCCGATGACCGGGGAGCCGGGCGCGGTGCACCTGCACCAGGATGCGTCGTGGTG 918 QY ,269 GluThrGluLysAsnAlaPheTyrAspGlnAsnAspGluTyrGlyMetSerThrLeuAla 288 11	ArgAsnTrp11eAlaGlyLeuLeuLysTyrValProGluAlaThrTyrPhePheAlaSer 30	309 TyrileAsnSerTyrLysArgLeuGlnProLeuThrPheAlaProThrLysCysCysTrp::: :::::
	873 GTCGCCGACCCGATGAAGGCCTGCGACTATGCGGTGCTGCTCAAGCGCCTGATCAAGAAC	OY 230 METALAGIUGINSETGIYMETVAIAIAINFPNEMETALALYSLEUSETSETTNIALAGUU 255 	256 GlyAsnAlaCysHisIleHisMetSerLeuGlnAspAlaGluThrGluLysAsnAlaPhe	276	696 'ACCAGCGAGGATCCCGAGCAGAACGCCGCATTGCGCCATGCGATCGGCGGGGGGGGGG	316 LeuGlnProLeuThrPheAlaProThrLysCysCysTrpAlaIleAspAsnArgThrSer	ON 336 AlaPheArgLeuCysAsnSerLysSerGluGlylleAsnValGluLeuArglleGlyGly 355 Oy 336 AlaPheArgLeuCysAsnSerLysSerGluGlylleAsnValGluLeuArglleGlyGly 355 Dh 52	356 AlaAspLeuAsnProTyrLeuAlaPheSerAlaIleIleAlaAlaGlyIleSerGlyIle		396 ProGluPheProAsnSerLeuGlnAsnAlaThrHisLeuLeuLysGluSerLysMetLeu 41	416 AsnLysThrPheGlyGluLysLeuIleLeuHisTyrValAsnAlaAlaAsnValGluIle	436 AsnGluPheSerLysGlnValThrAspTrpGluLeuAsn 448 125 GaGGATTTCAGTAGTTTCCAGTAGTTCCAGTAGTTTCCAGTAGTTTCCAGTAGTTTCCAGTAGTTTCCAGTAGTTCAGTAGTTCCAGTAGTTCCAGTAGTTCAGTAGTTCCAGTAGTTCCAGTAGTTCCAGTAGTTCAGTAGTAGTAGTTCAGTAGTTCAGTAGTTCAGTAGTTCAGTAGTAGTTCAGTAGTTCAGTAGTTCAGTAGTAGTTCAGTAGTAGTTCAGTAGTAGTTCAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTA	SULT 10 09-252-991A-11262	cation US/09252991A Rubenfield et al.	; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS ; FILE REFERENCE: 107196.136 ; CURRENT APPLICATION NUMBER: 118/09/252, 991A	CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18			Alignment Scores: 6.86e-43 Length: 1470 Pred. No.: 6.86e-43 Length: 1470 Score: 450.00 Matches: 130 Percent Similarity: 45.85% Conservative: 80

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1463
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                                                                                               AlalleSerAsnProHisAsnPheValThrSerGluProLeuPheCysSerProArgVal 120
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                                                                                                                                                                                                               GluLeuGluPheAsnLeuPheAsnGluThrTyrLysSerAlaSerGlnLysHisTrpLys 160
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                                                                                                                                                                                      ValTyrAsnAspLysGluLeuProGluPheProAsnSerLeuGlnAsnAlaThrHisLeu 408
                 AlalleAspAsnArgThrSerAlaPheArgLeuCysAsnSerLysSerGluGlyIleAsn 348
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APPLICANT: Rarbad, Arjan
APPLICANT: Rarbad, Arjan
APPLICANT: Rhodes, Michael J. C.
APPLICANT: Gasson, Michael J. APPLICANT: Walton, Nicholas J.
TITLE OF INVENTION: PRODUCTION OF VANILLIN.
FILE REFERENCE: 20747/100
CURRENT APPLICATION NUMBER: US/09/155,183
CURRENT FILING DATE: 1999-03-24
EARLIER APPLICATION NUMBER: PCT/GB97/00809
BARLIER PILING DATE: 1999-03-24
EARLIER FILING DATE: 1996-03-23
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
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Patent No. 6323011
GENERAL INFORMATION:
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Best Local Similarity:
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Pred. No.:
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Patent No. 6420135
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APPLICANT: Charles Kunsch
TITLE OF INVENTION: Strept
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR FILLING DATE: 1999-02-18
PRIOR FILLING DATE: 1998-07-18
PRIOR FILLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                  .701 AAGCGGGCCGAGCATGAAACTTCAAGCGCGTGATCAGCTCATGGGAA 1748
                                      AlaAsnValGluIleAsnGluPheSerLysGlnValThrAspTrpGlu
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Mismatches:
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                                                                                                                                                       Sequence 10987, Application US/09252991A Patent No. 6551795
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                                                                                                                                    US-09-252-991A-10987/c
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US-09-252-991A-10987
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LENGTH: 1425
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Sequence 1336, Application US/09134001C

Sequence 1336, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: LyAN DOUGETE-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR PEDLICATION NUMBER: US 60/064,964

PRIOR PEDLICATION NUMBER: US 60/055,779
  10606 GACTTGGCACCTACTGACCACACACACACGTCGTGAATGTCTTGACC 10547
                                                                                                         TIGGITCAGTGGATCCAATGGCGAACCCTTACGTTGCTATGGCTGTTCTTTTGGAAGTT 10010
                                                                                                                                                                                                     10316 GGTATTGCTGGATCAGGTATGCACTGTAATATGTCCTTGTTTGATGCAGAA---GGAAAT 10310
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10249 TTCCTAGGCGGTTTGATCAAGCATGCTTACAACTATCTGCCATCATGAACCCAACAGTT
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                                                                          GlualaglyIleLeuMetGlualaThrHisProGluPheLeuProSerGlnHisGluLeu
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11080 ATGCCAATCACAGCTGCAGATATTCGTCGTGAAGTCAAGGAAAAAAATGTTACCTTTATT 11021
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| 10822 AATGGAAGTGTTGCAGGTCTGTGATGTCTATACAACAGAAGGTGAACCATTTGCG 10763
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 ocrasion 6.2 ocravating System: MSDOS version 6.2 ocrawal and a soril Text current Application Data: APPLICATION DATA: APPLICATION NUMBER: US/08/961,527 classification NUMBER: US/08/961,527 prior APPLICATION NUMBER: US/08/961,527 prior APPLICATION NUMBER: Think Date: APPLICATION NUMBER: Think Date: ATPONCE, A. Anders Registration NUMBER: 36,373 reference/Docker, A. Anders Registration NUMBER: 36,373 reference/Docker, A. Anders Registration NUMBER: 984091 TELEPHONE: (301) 309-8504 TELEPHONE: (301) 309-8512 registration POR SEQ ID NO: 151: SEQUENCE CHARACTERISTICS:
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Mismatches:
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TYPE: nucleic acid
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US-09-252-991A-11454
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                                                                                                                                                                                                                                                                       GluGlyAlaValLeuAlaIleSerAsnProHisAsnPheValThrSerGluProLeuPhe 115
                                                                                                                                                                                                                                                                                                                                        GGTGATCCACGAGCTAACTTGAAGCGTGTATTAAGAAGAAGAATGGAAGATATGGGCTTTACT 399
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                                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                          Length:
Matches:
                                               TYPE: DNA
CRGANISM: Staphylococcus epidermidis
US-09-134-001C-1336
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1336
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409.00
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Best Local Similarity:
Query Match:
DB:
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                                      LENGTH: 1359
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APPLICANT: MARC J. Rubenfield et al.

APPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT PRESENCE: 107196-136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,120

PRIOR SEQ ID NOS: 33142
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                             369 AlaAlaGlyIleSerGlyIleGluGluLysLeuGluLeuProProAlaSerGlyAsn
                                                                                                                                                                                                                                                                                    LeuGlnAsnAlaThrHisLeuLeuLysGluSerLysMetLeuAsnLysThrPheGlyGlu
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US-09-252-991A-11454
; Sequence 11454, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
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356 CTGCTCAAGCGCCTGATCAAGAACATCGCCTACGACCACGAGATGGACACCACCTTCATG 415
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192 GluGluAla-----GlyIleLeuMetGluAlaThrHisProGluPheLeuProSer 208
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and is derived by analysis of the total score distribution
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-MODEL=frame+ p2n.model.-DBV=x1h
-Q-Cgn2_1/USFTO_spool/US10098602/runat_17122003_151235_28032/app_query.fasta_1.647
-Q=/cgn2_1/USFTO_spool/US10098602/runat_17122003_151235_28032/app_query.fasta_1.647
-Q=/cgn2_1/USFTO_spool/US10098602/runat_17122003_MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bite -GTRART=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=ptc -THR MAX=100 -THR_MIN=0 -ALIGNS=15
-MODE=LOCAL.-OUTFMT=ptc -NORM=ext -HRAPSIZE=500 -MINIEN=0 -MAXLEN=200000000
-USER=US10098602_@CGN 1_1 312_@runat_17122003_151235_28032 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NGG_SCORES=0 -WAIT -DSPEDCOK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -TRREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                              December 17, 2003, 22:45:30 ; Search time 394 Seconds (without alignments) 3110.520 Million cell updates/sec
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3165847 TTCGGCGAGGATGTTGTCGCGCACTACCTGAACACGCGCGTGTGGAGCTGGCGGCGTTC 3165788
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                           1166678 GCCACCGAGCTGGAGTTCATCGTGTTCGACCAGCCGTATCGCCAGGGATGGGCCAGCGGG
                                                                                                                                                                                                                                                                   ProleuThrMetAlaAspArgHisIleIleAlaLysHisGlyValArgGluMetAlaGlu
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AlaSerGluLeuGluPheAsnLeuPheAsnGluThrTyrLysSerAlaSerGlnLysHis
                                                                                                                   3166618 TATCGCGGGCTGACCCCGGCCAGCGACTACAACATCGACTACGCGATATTGGCATCCTCG
                                                                                                                                                             Gly11eGluThrPheMetArgSerValArgAsnLysLeuGluGluAlaGly11eLeuMet
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                                                                             TrpLysAsnLeuLysThrAlaGlnProHisHisGlnTrpMetAsnIleSerAlaSerSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium thuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and H37Rv (AA199682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6294328Bl.
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MetalaGluGlnSerGlyMetValAlaThrPheMetAlaLysLeuSerSerThrAlaLeu 255
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607 GATATCCAGCAT---CTARATGGCGAGCCGCTGAATCTTTCGCCTAGGAACCTTCTGCGT
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                                            LeuAspGlnLysLyslleSerIleSerThrPheValTyrAlaValThrIleGluGlyIle
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                                                                                                                                        L-alaninol; isopropylamine; iupI; ipuH; ofloxacin; ipuC; glutamylamide;
gamma-glutamylamide synthase; theanine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New microorganism for converting isopropylamine to L-alaninol, useful as pharmaceutical intermediate especially ofloxacin, has the ipuH and genes for alaninol catabolism inactivated -
                                                                                                                                                                                                                                                                                                                                                                                                                                          De Azevedo Waesch SI;
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                                                                                                            Pseudomonas sp KIE171-BII ipuC encoding DNA
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                                                                                                                                                                                                               Location/Qualifiers
283..1662
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/product= "ipuC"
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                    DNA; 1860
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                    AAI68686 standard;
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Maire T;
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:::::: 1174 ATGGTTGCGCTTGCCCGAGAAATGTCGGCCATCTATTTGCCGAATATCAACTCCTACAAG 1233 1294 GTATCGCACCGTGCGATTACATCAGCTGGCTCGCGCGGGGTCGAGAATCGGATCCCA 1353 1234 cecacescrescrescresces descentations de contra de c PheTyrAspGlnAsnAspGluTyrGlyMetSerThrLeuAlaArgAsnTrpIleAlaGly 294 315 ArgLeuGlnProLeuThrPheAlaProThrLysCysCysTrpAlaIleAspAsnArgThr 334 335 SeralaPheArgLeuCysAsnSerLysSerGluGlyIleAsnValGluLeuArgIleGly 354 375 IleGluGluLysLeuGluLeuProProProAlaSerGlyAsnValTyrAsnAspLysGlu 394 256 GlyAsnAlaCysHisIleHisMetSerLeuGlnAsp---AlaGluThrGluLysAsnAla 295 LeuLeuLysTyrValProGluAlaThrTyrPhePheAlaSerTyrIleAsnSerTyrLys 275 셤 ò 셤 ò ò 셤

313 AAGGTCCGAGATTTTATTGAGAAACACAATATCGACACGATTAGGCTGGGGGCGAGTCGAT 372

GluLeuAsnAsnLeulleArgAsnGlyLysileAspThrValValLeuAlaCysValAsp

US-10-098-602A-2 (1-454) x AAI68686 (1-1860)

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1860 159 73 194 31

Length: Matches: Conservative: Mismatches:

Percent Similarity: Best Local Similarity:

Query Match:

Indels: Gaps: MetGlnGlyArgLeuMetGlyLysArgLeuThrGlyArgHisPheLeu------Gly

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us-10-098-602a-2.rng

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----GACGGTTTGGAGTTTACTGGCTGGGATTCCGGGTATCCGGATATCGCCTTAATT 3006
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2833 AIAGAIGGAGICTGGCGCGAAGCAAGTIGGCGCAGAGIAITTCTIGAAIAAGGCGGCT
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                                                                                     GAAAGTGAAATGGCGCGAGTGATCTTCCCTAACGAGTTCGTTGAGCACTATGCCCAGATG 1587
1414 ATCGAAAATAAACTCAAGCCGAAAGATCCAATCCTCGGTAACGCTTAC-----AAAGTA 1467
                                                                 430
                                                                                                                                                                                                                                                                L-alaninol; isopropylamine; iupI; ipuH; ofloxacin; ipuC; glutamylamide; gamma-glutamylamide synthase; theanine; ipuB; ipuB; ipuE; ipuF;
                       SerLeuGlnAsnAlaThrHisLeuLeuLys
                                                                GluSerLysMetLeuAsnLysThrPheGlyGluLysLeuIleLeuHisTyrValAsnAla
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                                                                                                           AlaAsnValGluIleAsnGluPheSerLysGlnValThrAspTrpGluLeu
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'note= "Unidentified partial ORF,
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                     LeuProGluPheProAsn-
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Maire T;
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Length: Matches: Conservative: Mismatches: Indels:

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This invention describes novel microorganisms (A), or their enzymatic extracts, able to convert isopropylamine (I) to L-alaninol (II) and which have the ipuH and ipuI genes, encoding enzymes involved in metabolism of (II), inactivated. (II) is an intermediate for pharmaceuticals, especially ofloxacin. Also the enzyme encoded by the bacterial ipuC gene (a gamma-glutamylamide synthase) is used for synthesis of gamma-glutamylamides specifically theanine. Inactivation of the ipuH and I genes improves production of (II). Typically, a Pseudomonas in which both ipuH and I genes were inactivated produced (II) at 8 mM after 60 hour culture. For a similar strain in which only the ipuI had been inactivated the maximum (II) concentration was about 7 mM, after 6 hour, falling to practically zero after about 20 hour. This sequence encodes the Pseudomonas putida IpuB, IpuE, IpuE, IpuG and IpuH
                                                                                                                                                                                                                New microorganism for converting isopropylamine to L-alaninol, useful as pharmaceutical intermediate especially ofloxacin, has the ipuH and genes for alaninol catabolism inactivated
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                                                    AAG80037, AAG80038, AAG80039, AAG80040, AAG80041,
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Fig 3A-N; 106pp; German
                                                    P-PSDB; AAG80036, AAG80037, A
AAG80042, AAG80043, AAG80044.
WPI; 2001-626266/72.
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requences remassions represent una motecutes enconing and their associated DNA sequences immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and costeomyelitis), uvaltis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lessions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a text comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein cin the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). This sequence encodes the polypeptides shown in AAUS+556-AAUS+928 and AAUS+556-AAUS+556.

Copolypeptides shown in AAUS+56-AAUS+928 and AAUS+560-AAUS+556.

Contraction, but was obtained in electronic format directly from MIPO cat fitp.wipo.int/pub/published_pct_sequences.
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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'maisonneuve J, Zhang Y,
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WO200181581-A2
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ATCGAAAATAAACTCAAGCCGAAAGATCCAATCCTCGGTAACGCTTAC----AAAGTA 3927
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                                         MetalaGluGlnSerGlyMetValAlaThrPheMetAlaLysLeuSerSerThrAlaLeu
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AlaSerSerGlyIleGluThrPheMetArgSerValArgAsnLysLeuGluGluAlaGly
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AAS59566/
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polypeptides and nucleic acids useful for diagnosing infections, especially useful

Ä Bhatia

SS,

Mitcham JL, Wang St Jen S, Carter D;

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18847 ---CCGGCTGAAGTTGAGGGAGCTTTCGTTGAAGGCGTGGGCTTCGACGGCTCAGGTATC 18791
                                                                                                                                                                                                       18954 GCAGGCAGACTGAATTCGTCCTGCGTTCT-ATGGAGGAACGCAACATCCGTTTCGTAAGG
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187
51
Length:
Matches:
Conservative:
                                         Mismatches:
Indels:
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50.21%
31.30%
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T; 3 other;

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SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant; ds.

Propionibacterium acnes

Propionibacterium acnes immunogenic protein encoding DNA #61.

(first entry)

13-FEB-2002

AAS59566 standard; DNA; 34088 BP

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Brevibacterium lactofermentum; glnA2; glnE; L-glutamine; fermentation; coryneform bacterium; glutamine synthetase adenylyl transferase; glutamine synthetase; liver function promoting agent; enzyme; seasoning;
                                                                                                                                                                                               Brevibacterium lactofermentum glnA2 and glnE encoding DNA SEQ ID
                                                         GluileAsnGluPheSerLysGlnValThrAspTrpGluLeuAsnGln 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawashima H,
                                                                                                                                                                                                                                                                                                              Location/Qualifiers
659..1999
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                                                                                                                                                                                                                                                                                                                                                    "glnA2"
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                                                                                                                   BP.
                                                                                                                                                                                                                                                                                       Brevibacterium lactofermentum.
                                                                                                                   ABQ82091 standard; DNA; 5500
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Kurahashi O;
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                                                                                                                                                                               18625 AGGACGATGGGTCGTGCCGCAGAAATGGGTTTTACCTTCTATGTTCACCCAGAGATTGAG 18566
                                                                                                                                                                                                                                                                                    18523 GTGGCGCTGGACAACGGTGGCTACTTCGACCACCACCTTGGGAGCGGGCACCGACTTC 18464
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                                                                           18733 TTCCAAGTTCTGCCATGGCGTTCTGGCACCAGGACGCAGGATGTTCTGCGATATCACC 18674
                                                                                                                                                                                                                                  18565 TTCTACCTGCTTAACGAT------GAGCATCATCATCATCTGGGGAATCCCCG 18524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 TyrPhePheAlaSerTyrIleAsnSerTyrLysArgleuGlnProLeuThrPheAlaPro 323
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  --SerAspCysHisLeuCysAlaAspLeuAsnSer 88
                                                                                                                                                                                                                                                                                                                                                                               GAGGCCGCTCCTGGACAGCACGAAATTGACCTTCGTTACGCCGATGCGCTGACGATGGCC
                                                                                                      AsnProHisAsnPheValThrSerGluProLeuPheCysSerProArgValIleLeuMet
                                                                                                                                                                                                         PheAsnLeuPheAsnGluThrTyrLysSerAlaSerGlnLysHisTrpLysAsnLeuLys
                                                                                                                                                                                                                                                                                                            MetArgSerValArgAsnLysLeuGluGluAlaGlyIleLeuMetGluAlaThrHisPro
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                                                                                                                                                       124 GlnGlnIleGluArgLeuAlaAsnLeuLysLeuLysGlyLeuPheAlaSerGluLeuGlu
                                                                                                                                                                                                                                                                                                                                                               GluPheLeuProSerGlnHisGluLeuAsnPheValProAlaAspProLeuThrMetAla
                                                                                                                                                                                                                                                            164 ThrAlaGlnProHisHisGlnTrpMetAsnIleSerAlaSerSerGlyIleGluThrPhe
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                                                     LeuHisLeuLeuProTrpSerGluGlyAlaValLeuAla---
74 AspThrGlyTyr
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Nakamatsu T;

The present invention describes a coryneform bacterium (I) which has L-glutamine producing ability and has been modified so that its intracellular glutamine synthetase-activity-should be enhanced. Also described is a DNA (II) coding for a protein having glutamine synthetase activity or glutamine synthetase adenylyl transferase activity (see ABP53500 and ABP53501 respectively). (I) Is useful for producing accumulate L-glutamine in the medium and collecting the L-glutamine. L-glutamine in the medium and collecting the L-glutamine. L-glutamine produced by (I) is useful industrially as an ingredient of seasonings, as liver function promoting agents, in amino acid transfusions, and in comprehensive amino acid preparation. (II) is useful for breeding (I). The by-production of L-glutamic acid is suppressed and the production efficiency of L-glutamine is improved using (II). The present sequence encodes Brevibacterium lactofermentum glnA2 and glnE, which have glutamine synthetase activity and glutamine Coryneform bacterium which has L-glutamine producing ability and has been modified so that its intracellular glutamine synthetase activity should be enhanced, useful for producing L-glutamine Sequence 5500 BP; 1241 A; 1291 C; 1590 G; 1378 T; 0 other; synthétase adenylyl transferase activity respectively.

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1520 GTGACCAACCAGTGGGTCAATTCCTACAAACGCATCGTGTACGGAAACGAAGCTCCAACT 1579
                                                                                                      AATAAGGAGGAGTCGCCGGGGTGGGAGGTGCGTTTCCTGATACCGCTTGTAACCCATAT 1699
                                                                                                                                                    1760 GACGAGCCAGCTGAGGACGATATCTCCCAACTTGAGCTTCCGGGAACGTCGCGCCATGGGC 1819
                                                                                                                                                                                                                                                                                                                    1820 racaacear------creccaaacaccrrearcaecacrececcaaarg 1864
                                                                                                                                                                                                                                                                                                 410 LysGluSerLysMetLeuAsnLysThrPheGlyGluLysLeuIleLeuHisTyrValAsn 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                              AlaAlaAsnValGluIleAsnGluPheSerLysGlnValThrAspTrpGluLeuAsnGln
                                                                              SeriysSerGluGlyIleAsnValGluLeuArgIleGlyGlyAlaAspLeuAsnProTyr
                                                                                                                                   LeualapheSeralallelleAlaAlaGlyIleSerGlyIleGluGluLysLeuGluLeu
                                                                                                                                                                                                                                           TyrAsnAspLysGluLeuProGluPheProAsnSerLeuGlnAsnAlaThrHisLeuLeu
                                                                                                                                                                                         382 ProProAlaSerGlyAsnVal------
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                          LysCysCysTrpAlalleAspAsnArgThrSerAlaPheArgLeuCysAsn----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; SEQ ID NO: 2442; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glutamicum coding sequence fragment SEQ ID NO: 2442
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Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВБ.
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07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
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           The present invention provides a number of nucleotide and protein are queences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium of an organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
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528 AACATCATGACCTTCCGCTACATCATGAAACAGGTGGCAAGGGACCAAGGCGTCGGGGCA
                                                         ThrPheMetAlaLysLeuSerSerThrAlaLeuGlyAsnAlaCysHisIleHisMetSer
                                                                                                                                                                               LeuGlnAspAlaGluThrGluLysAsnAlaPheTyrAspGlnAsnAspGluTyrGlyMet
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225 ArgHisIleIleAlaLysHisGlyValArgGluMetAlaGluGlnSerGlyMetValAla 244 ACTGCACCTGGCCAGCAAGAATCGATTTACGCCATGCGGATGCGCTCACCATGGCCGAC 627

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111 SerGluProLeuPheCysSerProArgVallleLeuMetGlnGlnIleGluArgLeuAla 130
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                   pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine abses, nucleosides, nucleosides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.
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                                                                                                                                                                                                                                                                                                                    236 --------GAAGAGGCATCGGATTCGAT----------
                                                                                                                                                                                                                                                                                                                                            ValTyrAlaValThrileGluGlyIleAlaGlyGlyGlyTyrGluIleSerSerValAsp
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pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamic
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LeuGlnAspAlaGluThrGluLysAsnAlaPheTyrAspGlnAsnAspGluTyrGlyMet
                                                 SerThrLeuAlaArgAsnTrpIleAlaGlyLeuLeuLysTyrValProGluAlaThrTyr
                                                                           305 PhePheAlaSerTyrlleAsnSerTyrLygArgLeuGlnProLeuThrPheAlaProThr
                                                                                             962 GTGACCAACCAGTGGCTCAATTCCTACAAACGCATCGTGTACGGAAACGAAGCTCCAACT
                                                                                                                LysCysCysTrpAlalleAspAsnArgThrSerAlaPheArgLeuCysAsn-----
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                  TTATTTGAGGCGATACC----AACGCGTTCCACGATCCAGACGATTCTTACATGCTG
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                                                                                                                                                                                                                                  382 ProProProAlaSerGlyAsnVal--------
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Senoh A, Ikeda M, Ozaki A;
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ID AAH68531 standard; DNA; 349980 BP.
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                                                                                                                                                                                                                                                                             The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium coryneform bacterium and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium in the carbon in the sequence acids, nucleic acids, the present sequence is a nucleic acid described in the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 ArgSerValArgAsnLysLeuGluGluAlaGlyIleLeuMetGluAlaThrHisProGlu 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 ValTyrAlaValThrileGluGlyIleAlaGlyGlyGlyTyrGluIleSerSerValAgp
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                                                                                           mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 349980 BP; 80724 A; 98367 C; 90490 G; 80399 T; 0 other;
                                                                                                                                                                                                                         Disclosure; SEQ ID NO: 7066; 246pp + Sequence Listing; English.
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                                                             polynucleotides derived from Coryneform bacteria,
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2283649 ATGACAATCACAGCAGCAGCATCGTCGCGGACGTCAAGAAAAGGATATTAAATTCTTG 2283590
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                                                                                                                                                                                                                                                                                                            neguence (ARA90521) and related proteins (ARB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2365589 BP; 765914 A; 415261 C; 420487 G; 763927 T; 0 other;
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                                                                                                                                                                                                                      Lactococcus
                                                                                                                                                                                                                                                                                                   present invention is related to a Lactococcus lactis nucleotide
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                                                                                                                                                                                                                    New nucleotide sequence useful in the identification or lactis and related species \mbox{-}
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2283481 TCAATCGAAGGATTC-----
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Query Match:
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                                                                    263588 ACTGCACCTGGCCAGCAAGAAATCGATTTACGCCATGCGGATGCGCTCACCATGGCCGAC
                                                                                                                                                                                          263408 TTATTTGAGGGGGTACC----AACGCGTTCCACGATCCAGACGATTCTTACATGCTG
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263054 GACGAGCCAGCTGAAGACGATGAGCTTCCGGGAACGTCGCGCCATGGGC
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                                                                                                             225 ArgHisIleIleAlaLysHisGlyValArgGluMetAlaGluGlnSerGlyMetValAla
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                                               205 PheLeuProSerGlnHisGluLeuAsnPheValProAlaAspProLeuThrMetAlaAsp
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Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1104

Bifidobacterium longum NCC2705; Bifidobacterium; bacterial; antidiarrheic; antibacterial; inhibitor of Salmonella; detection; identification; lactic acid bacterium; diarrhoea; pathogenic bacteria; rotavirus; food composition; pharmaceutical composition; gene; ds.

Bifidobacterium longum.

Synthetic.

EP1227152-A1

31-JUL-2002

30-JAN-2001; 2001EP-0102050.

2001EP-0102050

30-JAN-2001;

(NEST) SOC PROD NESTLE

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2283184 GGTTATTTTGACCTTGCACCAACTGACCTCGCTGGAAACACACAGAGGGGGAAATCGTAAAT 2283125
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 2283280 GGCTTCAAGAGCTTTAACCTTGGACCTGAACCAGAGTTCTTCCTTTTCAAACTTAATGAA 2283221
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                                                                                              170 GlnTrpMetAsnIleSerAlaSerSerGlyIleGluThrPheMetArgSerValArgAsn
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                                                            2283220 AATGATGAACCAACACTTGAAGTGAATGATAAAGGT----
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The present invention describbes a polynucleotide a gequence of a Bifidobacterium genome selected from the mucleotide acquence given in ABQ81842 and ABQ81843, or a sequence exhibiting at least 90% identity or which hybridises with the sequence exhibiting at least 90% identity or which hybridises with the sequence exhibiting at least 90% identity or which hybridises with the sequence exhibiting a fusion protein, comprising a sequence selected from 1097 sequences given in ABB6528 to AB66534 ligated in frame to a polynucleotide [II] encoding a heterologous polypeptide. (I) has antidiarrheic_and activities, and can be used as an inhibitor of Salmonella. (I) which is a probe) is useful for the detection and/or identification of Bifidobacterium Bifidobacterium longum in a biological sample. A carrier ontaining the lactic acid bacteria and/or recating diarrhoea brought about by pathogenic bacteria and/or rotavirus. The carrier is a food composition selected from milk, yogurt, cutd, cheese, fermented milks, milk based fermented products, ice-creams, fermented cereal based products, milk based for tablets, infant formula, pet food or a pharmaceutical composition selected from tablets, liquid bacterial suspensions, dried oral supplement, wet oral supplement, dry tube feeding or wet tube feeding.

(I) is useful in DNA arrays or chips to carry out analysis of the bifidobacterium related nucleotide sequences given in the Sequence interesting from the present invention but not mentioned further within the contraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --ThrGlyTyrSerAspCys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polynucleotide comprising Bifidobacterium genome sequence useful as a probe or primer for detecting and/or identifying Bifidobacterium longum in a biological sample
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention describes a polynucleotide (I) comprising
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31.05%
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Best Local Similarity:
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BP.

DNA; 349980

standard;

ABQ81848 ABQ81848; (first entry)

19-NOV-2002

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MetThrIleThrTyrAspGluLeuAspAsnLeuIleArgAsnGlyLysIleAspThrVal 20
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The method comprises exposing trans-ferulic acid, or its salts, to trans-ferulate:CASH ligase, trans-feruloyl SCOA hydratase and 4-hydroxy-3-methoxyphenyl-beta-hydroxypropionyl-S-COA cleavage activities. A similar novel method in which vanillin is converted covanillic acid, or its salts, utilises a 4th enzyme, especially vanillin achid can be used to make oligomers, or as a monomer of vanillin acid can be used to make oligomers, or as a monomer of polyesters. By expressing vanillin in plants or food-grade microorganisms, vanillin is generated in situ during preparation of fermented foods and beverages. Transgenic plants, particularly food plants, may be able to produce other particularly food plants, may be able to produce other can ompounds in addition to vanillin. This method is less expensive than extraction from Vanilla pods, and generates a mail are to natural vanilla pod extract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of vanillin from trans-ferulic acid using 3 enzymes - followed by oxidation to vanillic acid, useful as a food
                                                                                                                                                                                                                                                                                                                                                                                         product/pF1901; vanillin product
production; food flavouring; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus, GAS, GBS, group B streptococcus, Streptococcus agalactiae, group A streptococcus, Streptococcus pyogenes, antibacterial, gene, antiinflammatory, infection, vaccine, meningitis, gene therapy, ds.
                                                                                                                                   Gly11eSerGly11eGluGluLysLeuGluLeuProProProAlaSerGlyAsnValTyr
                                                                                                                                                                                                                                                 391 AsnAspLysGluLeuProGluPheProAsnSerLeuGlnAsnAlaThrHisLeuLeuLys
                                                                                                                                                                                                                                                                                                                                     1584 GAGCGCGCAACCTG---CGTCTGCCGCTGACCATCGAAGACGCTCTGGAACGCATGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                        411 GluSerLysMetLeuAsnLysThrPheGlyGluLysLeuIleLeuHisTyrValAsnAla
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or disease caused by Streptococcus bacteria, such as meningitis,
for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               431 AlaAsnValGluIleAsnGluPheSerLysGlnValThrAspTrpGlu 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus polynucleotide SEQ ID NO 4899.
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24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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                                                                                                                                                                                                                                                                                                            ThrLysCysCysTrpAlalleAspAsnArgThrSerAlaPheArgLeuCysAsnSerLys 343
                                                                                                                                                                                                                                                                                                                                              GTTTACGTTGCTTGGGAGGTCGCAATCGTTGCTATTCGTGTACCTGCATCTCGA 990
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                                       TTTGATAATGAA---GGGAACAATGCTTTCTTTGATCCAGAAGATCCACGTGGAATGCAA
                                                                                                                                 GCTATCATTAATCCAACTGTTAATTCTTATAAACGTTTGGTACCAGGATACGAAGCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                          344 SerGluGly1leAsnValGluLeuArg1leGlyGlyAlaAspLeuAsnProTyrLeuAla
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                                                                                       ---SerThrLeuAlaArgAsnTrpIleAlaGlyLeuLeuLysTyrValProGluAlaThr
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              Streptococcus polynucleotide SEQ ID NO 10967.
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Tettelin H;
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|TCTGATATGTATTTATATCCTGATTTAGATACTTGGATTGTCTTTCCTTGGGGAGATGAA 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGTTTGATGTTCACAGATATCTTAGGAGTAATGAAAATGTCGAAATTCCG----- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GCTACAGATGAACAATTAGACAAGTTTTATCAAATAAAGCAATGTTTGATGGA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---GlyAlaValLeuAlaIleSerAsnProHisAsnPheValThrSerGluProLeuPhe 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   MetThrileThrTyrAspGluLeuAsnAsnLeuIleArgAsnGlyLysIleAspThrVal 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValleuAlaCysValAspMetGlnGlyArgLeuMetGlyLysArgLeuThrGlyArgHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValThrileGluGlyIleAlaGlyGlyGlyTyrGluIleSerSerValAspThrGlyTyr 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||| ::: ::||||::: GGAGATCTTAAGCGTAATATGAAACGTATGCAAGAGATGGGCTATAAG
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chromatography, immunoassays, and distinguishing/identifying Streptococcus proteins.
                                                                                                                      277 G; 417 T; 0 other
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131
80
213
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Matches:
Conservative:
Mismatches:
Indels:
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445.00
44.14%
27.41%
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-----GCTACAGATGAACAATTAGACAAGTTTTATCAAATAAAGCAATGTTTGATGGA 1725892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----AAAATGGATGAAAATGGTAACCCAACACTTGATGTT 1725604
                                                                                                         Etreptococcus (GBS (Streptococcus againstant) And Strengtococcus (GBS) (Streptococcus againstant) And Strengtococcus (GBS) (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABMS6044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to U). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---GlyAlaValLeuAlaIleSerAsnProHisAsnPheValThrSerGluProLeuPhe 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CysSerProArgValIleLeuMetGlnGlnIleGluArgLeuAlaAsnLeuLysLeuLys 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyLeu---PheAlaSerGluLeuGluPheAsnLeuPheAsnGluThrTyrLysSerAla 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MetThrileThrTyrAspGluLeuAsnAsnLeuIleArgAsnGlyLysIleAspThrVal 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ValleuAlaCysValAspMetGlnGlyArgLeuMetGlyLysArgLeuThrGlyArgHis 40
o' Streptococcus protein for the treatment or prevention of infection disease caused by Streptococcus bacteria, such as meningitis, and detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                             acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 ValThrileGluGlyIleAlaGlyGlyGlyTyrGluIleSerSerValAspThrGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PheLeuGlyLeuAspGln-----LysLysIleSerIleSerThrPheValTyrAla
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2155561 BP; 695741 A; 385320 C; 382958 G; 691542 T; 0 other;
                                                                                                 relates to a protein (ABP25413-ABP30895) from group B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1725996 CGTTTGATGTTCACAGATATCTTAGGAGTAATGAAAAATGTCGAAATTCCG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1725678 TCATTTAACTTAGGACCAGAACCTGAATTTTTCCTATTT
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Mismatches:
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                                                                Claim 8; Page 4196-4488; 4525pp; English.
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445.00
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27.41%
                                                                                                                                                                                                                                                                                                                                                                  Streptococcus proteins.
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1725126 GTTTACGTTGCTTGGCAGTCGCAATCGTTGCCCACTTATTCGTGTACCTGCATCTCGA 1725067
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                                                                                                SerValArgAsnLysLeuGluGluAlaGlyIleLeuMetGluAlaThrHisProGluPhe
                                                                                                                                                                                                                             · 206 LeuProSerGlnHisGluLeuAsnPheValProAlaAspProLeuThrMetAlaAspArg
                                                                                                                                                                                                                                                                                                                                                                226 HisIleIleAlaLysHisGlyValArgGluMetAlaGluGlnSerGlyMetValAlaThr
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949 GGAAGTAATCGTTCACCGTTATCCGTGTTCCAGCATCACGTGGTATGGGAACGCGTTTG 1008
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| 1189 CATÀATGCCTTAAAAGGTCTTTCAAAAAGATGATGTGGTACAAAAGGCACTAGGTTACCAT 1248
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                                                                                                                                                                                       ArgValileLeuMetGlnGlnIleGluArgLeuAlaAsnLeuLysLeuLysGlyLeu--- 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    889 Grgadriciraradacearraceacrecaegrangaegecaecrerrangecer
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|1129 IATACCATGACAATGAAGGAAATGAAGCAGGCATTATTGATTTGCCATCAACGCTT
                                                                                            ValLeuAlaIleSerAsnProHisAsnPheValThrSerGluProLeuPheCysSerPro
                                                                                                                                                                                                                  HisLeuCysAlaAspLeuAsnSerLeuHisLeuLeuProTrpSerGlu-----GlyAla
                                              208 TACCTTTACCCCGATTTAGACACTTGGATTGTTTTTCCCTGGGGAGATGAAAATGGAGCA
                                                                                                                                      GTTGCAGGTTTAATTTGTGATATTTATACAGCAGAAGGAAAGCCTTTTGCAGGAGATCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5481 sequences (S1), given in the specification. The proteins have antibacterial and antihiflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and thodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a streptococcus mapple. (I) is used to detect Streptococcus in a composition comprising (I) or a nucleic acid encoding (I) may be used to accombinantly produce (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity contours and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GTACGGATCAATGAGTCAGATATG 207
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(GENO-) INST GENOMIC RES.
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    Streptococcus pyogenes
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Sequence 1, Appli Sequence 1018, A Sequence 752, App Sequence 151, App Sequence 311, App Sequence 211, App Sequence 112, App Sequence 112, App Sequence 112, App Sequence 12996, A Sequence 12996, A Sequence 2935, Appl Sequence 28, Appl Sequence 27, Appl

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

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11 BELHALVAGGEIDTVVLAFPDMQGRLQGKRFAARFFL---DEVLEHGTEGCNYLLAVDTD
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            US-10-299-799-1

US-09-815-72-10418

US-10-156-72-10418

US-10-205-823-15-2

US-10-304-749-3166

US-094-749-3166

US-09-815-242-5216

US-09-711-161A-241

US-09-771-161A-241

US-09-810-937-10

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US-10-272-502A-22
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GENERAL INFOGRALION:
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: BISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: SAKAKI, NASAHIRA
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
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Watches 175; Conservative
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score greater than or equal to the score of the result being printed
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
              version 5.1.6
- 2003 Compugen Ltd.
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5 US-10-062-458-2

US-09-815-242-13378

5 US-10-156-761-13481

US-09-815-242-1338

US-09-815-242-12338

US-09-815-242-12738

US-09-815-242-12775

US-09-815-242-11338

US-09-815-242-11332

US-09-815-242-11332

US-09-815-242-11332

US-09-815-242-11332

US-09-815-242-11363
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Maximum Match 100%
Listing first 45 summaries
                                                                               - protein search, using sw model
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              GenCore (c) 1993
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seq length: 200000000
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Match Length
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773.5 475.5 470.5 432 427.5 424.5 424.5 402

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322 291 287 281.5 265.5

121

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12;
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                                                                                                                                                         LAFSAIIAAGISGIEEKLELPPPASGNV------YNDKELPEFPNSLQNATHLL 409
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TFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLARNWIAGLLKYVPEATY
                                                                                                     288 VINQWVNSYKRIVYGNEAPIAATWGVSNRSALVRVPIYRLNKEESRRVEVRLPDIACNPY
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                                     230 SFMPKPFQEHAGSAMHTHMSLFEGDT--NAFHDPDDSYMLSKTAKQFIAGILHHAPEFTA
                                                                              305 FFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCN---SKSEGINVELRIGGADLNPY
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                                                                                                                                                                                                                                        410 KESKMLNKTFGEKLILHYVNAANVEINEFSKQVTDWELNOGFN 452
                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 5942, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
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ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
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Best Local Similarity
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US-09-738-626-5942
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APPLICANT: NAKAMURA, JUN
APPLICANT: NAKAMURA, JUN
APPLICANT: MORIGUCHI, KAYO
APPLICANT: MORIGUCHI, KAYO
APPLICANT: MORIGUCHI, KAYO
APPLICANT: MAKAMATSU, TSUYOSHI
TITLE OF INVENTION: METHOD FOR PRODUCING L-GLUTAMINE BY FERMENTATION AND L-GLUTAMINE
TITLE OF INVENTION: METHOD FOR PRODUCING BACTERIUM
FILE REFERENCE: 219181USO
CURRENT APPLICATION NUMBER: US/10/062,458
CURRENT APPLICATION NUMBER: US/201-28163
PRIOR APPLICATION NUMBER: JP 2001-28163
PRIOR APPLICATION NUMBER: JP 2001-162806
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VERSION 3.1
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                                                                                                                                                                                  242 MVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLARNWIAGLLKYVPE 301
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                        LMQQ1ERLANLKLKGLFASELEFNLFNETYKSASQKHWKNLKTAQPHHQWMNISASSGIE 181
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                                             247 VSITFWAKYNERE-GNSCHIHLSLADAD-GTNAMAGDGPG-GMSDVWRHFLAGQLAALRD
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29.2%; Pred. No. 1.2e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                          KLILHYVNAANVEINEFSKOVTDWELNQGFNR 453
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Publication No. US20030003550Al
GENERAL INFORMATION:
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Best Local Similarity
Matches 135; Conserv
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61 EGIAGGGYEISSVDTGY-SDCHLCADLNSLHLLPWSEGA-----VLAISNPHNFVTSEP 113
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                                                                                                                                                                                                             STLARNWIAGLLKYVPEATYFFASYINSYKRLQPLT-----FAPTKCCWAIDNRTSA 336
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                                                                                           291 WIAGLLKYVPEATYFFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCNSKSEGINVE
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Pred. No. 1.3e-35;
74; Mismatches 167; Indels
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APPLICANT: SHIBA, TADAYCSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
SROID NO 13481
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13481, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-13481
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30.0%;
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
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Best Local Similarity 30.09
Matches 127; Conservative
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                                                                                         LAFSAIIAAGISGIEEKLELPPPASGNV-----YNDKELPEFPNSLQNATHLL 409
                                                                                                                                LAFSVMLGAGLKGIKEGYELDEPAEDDISNLSFRERRAMGYND-----LPSSLDQALRQM 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 VTIEGIAGGGYEISSVDTGYSDCHLCADLNSLHLLPWSE--GAVLAISNPHNFVTSEPLF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 CSPRVILMQQIERLANLKLKGL-FASELEFNLF--NETYKSASQKHWKNLKTAQPHHQWM 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 GDPRGNLKRALRHMEEVGFKSFNLGPEPEFFLFKLDENGDPTLEVNDKG------GYF 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NISASSGIETFMRSVRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTMADRHIIAKHG 232
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FFASYINSYKRLOPLTFAPTKCCWAIDNRTSAFRLCN---SKSEGINVELRIGGADLNPY
                                           288 VTNOWVNSYKRIVYGNEAPTAATWGVSNRSALVRVPTYRLNKEESRRVEVRLPDTACNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MTITYDELNNLIRNGKIDTVVLACVDMQGRLMGKRLTGRHFLGLDQ---KKISISTFVYA
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                                                                                                                                                                                                                KESKMLNKTFGEKLILHYVNAANVEINEFSKOVTDWELNOGFN 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Essential Genes
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18.2%; Score 432; DB 9; L
Best Local Similarity 27.2%; Pred. No. 4.4e-36;
Matches 128; Conservative 83; Mismatches 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Identification of Esse
TITLE OF INVENTION: Prokaryotes .
FILE REFERENCE: ELITRA.OILA
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                Sequence 13378, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptococcus pneumoniae US-09-815-242-13378
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto, Robert T.
Xu, H. Howard
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305
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AGLLKYVPEATYFFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCNSKSEGINVELR 352
                                          278 AGVLKNARGFTAVCNPLVNSYKRLVPGYEAPCYIAWSGKNRSPLIRVPSSRGLSTRIEVR 337
                                                                                                  353 IGGADLNPYLAFSAIIAAGISGIBEKLELPPPASGNVY--NDKE-----LPEFPNSLQNA 405
                                                                                                                             338 SVDPAANPYMALAAILEAGLDGIKNKLKVPEPVNQNIYEMNREERBAVGIQDLPSTLYTA 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 GIAGGGYEISSVDTGYSDCHLCADLNSLHLLPWS--EGAVLAISNPHNFVTSEPLFCSPR 119
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                                                                                                                                                                                                        THILKESKMINKTFGEKLILHYVNAANVEINEFSKOVTDWELNOGFNRY 454
                                                                                                                                                                                                                                      398 LKAMRENEVIKKALGNHIYNQFINSKSIEWDYYRTQVSEWERDQYMKQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: AYRING, JUGATEN W.
APPLICANT: AYRING, JOHN D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
CURRENT FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-112-22
PRIOR FILING DATE: 2000-112-22
PRIOR FILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SSOFTWARE: FERSEEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12338, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohlsen, Kari L.
Zyskind, Judith W.
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                             VREMAEQSGMVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLARNWI 292
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  DKE-----LPEFPNSLQNATHLLKESKMLNKTFGEKLILHYVNAANVEINEFSKQVTDWE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.9%; Score 424.5; DB 9;
26.2%; Pred. No. 2.7e-35;
ive 92; Mismatches 211;
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ohleen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essent:
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
FILING APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 601191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5733
LENGTH: 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                        Sequence 5733, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Staphylococcus aureus US-09-815-242-5733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 26.2%;
Matches 123; Conservative
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                                                                                                        LNQ 449
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173 NISASSGIETFMRSVRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTMADRHIIAKHG 232
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                                                                                                                                                                                                                                                                                                                 338 SVDPAANPYMALAAILEAGLDGIKOKLKVPEPVNQNIYEMNREEREAVGIQDLPSTLYTA 397
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                                                                                                                                                                                       293 AGLLKYVPEATYFFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCNSKSEGINVELR
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                                                                                                                                                                                                                                                                                                                                                                            406 THLLKESKMLNKTFGEKLILHYVNAANVEINEFSKOVTDWELNOGFNRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-00-23
PRIOR PILING DATE: 2000-010-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/259,931
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
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                                                                                                                                                                                                                  278 AGVLKNARGFTAVCNPLVNSYKRLVPGYEAPCYIAMSGKNRSPLIRVPSSRGLSTRIEVR 337
                                                                                          AGLLKYVPEATYFFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCNSKSEGINVELR 352
                                                                                                                                                                                     353 IGGADLNPYLAFSAIIAAGISGIEEKLELPPPASGNVY--NDKE-----LPEFPNSLQNA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 GIAGGGYEISSVDTGYSDCHLCADLNSLHLLPWS--EGAVLAISNPHNFVTSEPLFCSPR 119
VREMAEQSGMVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLARNWI 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 VILMQQIERLANLKLKGL-FASELEFNLFNETYKSASOKHWKNLKTAQPHHQ-----WM 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GEPTLELNDDGGYF 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 TFTKDDIRKFAEEENVRYLRLQFTDILGTIKNVEVPVSQL----EKVLDNEMMFDGSSIE
                             398 LKAMRENEVIKKALGNHIYNQFINSKSIEWDYYRTQVSEWERDQYMKQY 446
                                                                                                                                                                                                                                                                               406 THLLKESKMLNKTFGEKLILHYVNAANVEINEFSKOVTDWELNOGFNRY 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9; Length 446;
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.9%; Score 424.5; DB 9; 26.2%; Pred. No. 2.7e-35; tive 92; Mismatches 211;
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/25,578
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257
PRIOR APPLICATION NUMBER: 60/257
PRIOR APPLICATION NUMBER: 60/257
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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Best Local Similarity 26.2%
Matches 123; Conservative
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170 KVRYKGGYFPTPPVDHFADLRAEISLE-----LANSGLQVERQHHEVGTAGQAEIN 220
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                                                                                                         YDONDEYGMSTLARNWIAGLLKYVPEATYFFASYINSYKRLOPLTFAPTKCCWAIDNRTS 335
                                                                                                                                                                                               336 AFR--LCNSKSEGINVELRIGGADLNPYLAFSAIIAAGISGIEEKLELPPPASGNVY--- 390
                                                                                                                                                                                                                           66 GGYEISSVDTGY-SDCHLCADLNSLHLLPWSEGAVLAIS-NPHNFVTSEPLFCSPRVILM 123
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                                                                                                                                     PADPLTMADRHIIAKHGVREMAEQSGMVATFMAKLSSTALGNACHIHMSLQDAETEKNAF
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                                                            231 FNTMLHAADDIQTFKYIIKNTARLHGKAATFMPKPLAGDNGSGMHAHQSLW--KDGKPLF
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                                                                                                                                                                                                                                                                                                                    PEEAASIPQAPISLEASLKALQEDTDFLTESDV----FTEDLIEAYI 451
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; Pred. No. 2.8e-21;
68; Mismatches 189;
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APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
FRIOR PELICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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HORIKAWA, HIROSHI
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Best Local Similarity 25.9°
Matches 113; Conservative
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US-10-156-761-13532
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                                                                                                                  239 MPKPLFGINGSGMHCNMSL--FNEEGNVFYDESGEMGLSQTAYHFLGGLLKHARAYTAVC 296
VRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTMADRHIIAKHGVREMAEQSGMVATF 246
                                       179 IVLELESLGFEVEASHHEVAPGQHEIDFKYADVVDACDNIQTFKLVVKTIARKHGLHATF 238
                                                                                      247 MAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLARNWIAGLLKYVPEATYFF 306
                                                                                                                                                                            307 ASYINSYKRLOPLTFAPTKCCWAIDNRTSAFRLCNSKSEGINVELRIGGADLNPYLAFSA 366
                                                                                                                                                                                                                      297 NPTVNSYKRLVPGYEAPVYVAWSGRNRSPLIRVPESRGLSTRLELRSVDPSANPYLTMAV 356
                                                                                                                                                                                                                                                                     367 IIAAGISGIEEKLELPPPASGNVY--NDKE----LPEFPNSLQNATHLLKESKMLNKTF 419
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Corynebacterium glutamicum
US-09-738-626-6985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6985, Application US/09738626 Publication No. US20020197605A1 Publication No. US20020197605A1 APPLICANT: NAKAGAWA, SATOSHI
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ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
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TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
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Best Local Similarity 26.64
Matches 124; Conservative
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332 NRTSAFRL-CNSKSEGINVELRIGGADLNPYLAFSAIIAAGISGIEEKLELPPPASGNVY 390
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APPLICANT: Paradkar, Ashish
APPLICANT: Paradkar, Ashish
APPLICANT: Varoglu, Mustafa
APPLICANT: Varoglu, Mustafa
APPLICANT: Wathur, Eric J.
TITLE OF INVENTION: GLYCOSYLATED KINAMYCINS AND METHODS OF
TITLE OF INVENTION: MAKING AND USING THEM
FILE REPERENCE: 09010-280001
CURRENT APPLICATION NUMBER: US/10/187,267A
CURRENT APPLICATION NUMBER: US 60/301,401
PRIOR FILING DATE: 2001-06-27
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.8%; Score 281.5; DB 15; Length llarity 25.1%; Pred. No. 3e-20; Conservative 77; Mismatches 210; Indels
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                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 57, Application US/10187267A; Publication No. US20030124679A1; GENERAL INFORMATION:
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122; Conserv
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Best Local S
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TSAFR--LCNSKSEGINVELRIGGADLNPYLAFSAIIAAGISGIEEKLELPPPASGNVY- 390
                              SAAMRIPITGSNPKAKRVEFRAPDSSGNPYLAFSALLLAGLDGIKNKVEPAEPIDKDLYE 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 -PRVILM--QQIERLANLKLKGLFASELEFNLFNETYKSAS------QKHWK-NL 162
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APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: You Howard
CURRENT FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11137
LENGTH: 472
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Best Local Similarity
Matches 116; Conserv
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325 KCCWAIDNRTSAFRL-CNSKSEGINVELRIGGADLNPYLAFSAIIAAGISGIEEKLELPP 383
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                                                                                                                                                                  392 AADKNLYDLPPEEAKEIPQVCGSLKEALBELDKGRAFLTKGGVFTDEFIDAYIELKSEE 450
                                                                                                                          384 PASGNVYN-----DKELPEFPNSLQNATHLLKESK-MLNK--TFGEKLILHYVNAANVE 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Walking Juditon W.
APPLICANT: Walking Juditon W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamanto, Robert T.
APPLICANT: Yamanto, Robert T.
APPLICANT: Yamanto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PRILING DATE: 2000-05-26
PRIOR PRILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-12-26
PRIOR FILING DATE: 2000-12-26
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                  Sequence 11507, Application US/09815242
Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zyskind, Judith W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohlsen, Kari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 LQDAETEKNAFYDQNDEYGMSTLARNWIAGLLKYVPEATYFFASYINSYKRLQPLTFAPT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 PSTMOGYERDPRNIAKRAEEYLKSTGIGDTVFVGPEPEFFIFDBVKFKSDISGSMFKIFS 154
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                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CALIBEN, MAIL Daniel
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Derokaryotes
FILE OF INVENTION: Derokaryotes
FILE OF INVENTION: Prokaryotes
FILE OF INVENTION: Date: 2001-03-21
FRIOR APPLICATION NUMBER: 60/191,078
FRIOR PELING DATE: 2000-03-21
FRIOR PELING DATE: 2000-05-26
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR APPLICATION NUMBER: 60/253,625
FRIOR PELING DATE: 2000-10-23
FRIOR PELING DATE: 2000-11-27
FRIOR APPLICATION NUMBER: 60/253,625
FRIOR APPLICATION NUMBER: 60/253,33
FRIOR APPLICATION NUMBER: 60/257,931
FRIOR APPLICATION NUMBER: 60/257,931
FRIOR APPLICATION NUMBER: 60/257,931
FRIOR FILING DATE: 2000-12-216
FRIOR FILING DATE: 2000-12-216
FRIOR FILING DATE: 2001-02-16
FRIOR APPLICATION NUMBER: 60/257,931
FRIOR FILING DATE: 2000-12-216
FRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                       Sequence 12088, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                            Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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Best Local Similarity 24.8*
Matches 119; Conservative
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495 EYFEAF 500
   449 QGFNRY 454
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Sequence 17901, A
Sequence 27559, A
Sequence 28048, A
Sequence 27833, A
Sequence 4173, Ap
Sequence 19014, A
Sequence 16796, A
Sequence 18960, A
Sequence 18960, A
Sequence 18960, A
Sequence 28811, A
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Sequence 6200, Ap
Sequence 4580, Ap
                                                                                                                                                   December 17, 2003, 22:43:05; Search time 19 Seconds (without alignments) 1011.007 Million cell updates/sec
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/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-09-252-991A-27559

US-09-252-991A-27833

US-09-252-991A-27833

US-09-252-991A-19014

US-09-252-991A-19014

US-09-252-991A-19014

US-09-252-991A-18960

US-09-252-991A-18960

US-09-252-991A-18960

US-09-328-352-4633

US-09-328-352-4633

US-09-328-352-4633

US-09-328-352-4633

US-09-328-352-4630

US-08-471-044-50

US-08-471-044-50

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US-09-028-366-3
US-09-252-991A-29534
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match I
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JS-09-134-001C-5311 Sequence 5311, Ap	-08-335-865J-21 Sequence 21, Appl	Sequence 8,	Sequence 9,	US-09-134-001C-3159 Sequence 3159, Ap	-09-134-001C-4383 Sequence 4383, Ap	-09-328-352-4551 Seguence 4551, Ap	Sequence 16	Sequence 3,	-09-370-700-3 Sequence 3, Appli	Sequence 3,	Sequence 75	-09-328-352-7993 Sequence 7993, Ap	-09-328-352-5599 Sequence 5599, Ap	Seguence 4,	Seguence	-09-328-352-5486 Sequence 5486, Ap	Sequence
SD	ns	S	S	S	nS	S	S	SD	S	ns	S	SD	ns	ns	ns	Sn	nS
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461	593	1013	995	10182	. 506	952	731	2152	2152	2152	441	299	733	1074	609	3290	973
3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.6	3.6	3.6
91	91	91	90	90	89.5	89.5	88.5	88	88	88	87.5	87	87	87	86.5	86.5	86
. 8	59	30	31	32	33	34	35	36	37	38	39	0	11	12	13	4	12

ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCUEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 CHLCADLNSLHLLPWSEGAVLAISNPHNFVTSE-----PLFCSPRVILMQQIERLANL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 KLKGLFASELEFNLF-----NETYKSASQKHWKNLKTAQPHHQWMNISASSGIETFWRS 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 MAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLARNWIAGLLKYVPEATYFF 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          307 ASYINSYKRLOPLTFAPTKCCWAIDNRTSAFRLCNSKSEGINVELRIGGADLNPYLAFSA 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.2%; Score 481; DB 4; Length 449; 28.9%; Pred. No. 2.2e-44; Indels iive 94; Mismatches 181; Indels
                                      Sequence 17901, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17901
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 28.9%
Matches 128; Conservative
RESULT 1
US-09-252-991A-17901
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Gaps

us-10-098-602a-2.rai

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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: A RENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: A RENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT FILLING DATE: 1999-02-18
PRIOR PRILICATION NUMBER: US 60/074,788
PRIOR PRILICATION NUMBER: US 60/094,190
PRIOR FILLING DATE: 1998-02-18
PRIOR FILLING DATE: 1998-02-18
SEQ ID NOS: 33142
SEQ ID NO 28048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS.

FILE REFERENCE: 107196.18

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27833

LENGTH: 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLKLKGLFASELEFNLFN-ETYKSASQKHWKNLKTAQPHHQWMNISASSGIETFMRSVRN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 EMELTIVAAFELEFYLIDQENVNGRPOPPRSPISGKRP--QSVQVYSIDDLDEYVECLQD 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLEEA---GILMEATHPEFLPSQHELNF-VPADPLTMADRHIIAKHGVREMAEQSGMVAT 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 SVDTGYSDCHLCADL-NSLHLLPWSEGAVLAISNPHNFVTSEPLFCSPRVILMQQIERLA
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FMAKPYPGQAGNGLHVHISLLD-KHGNNIFTSEDPE--QNAALRHAIGGVLETLPASMAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 455; DB 4; Length 46; Pred. No. 1.9e-41; 86; Mismatches 211; Indels
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; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28048
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28.0%;
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 10196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PRILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27559
LENGTH: 464
                                                                   363 SLAAGLYGLEHELE-PSPA---IQGEFEVPEELTLPCTMYDALRRLKGSALARELFGSEF 418
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                                             1 I AAGISGIEEKLELPPPASGNVYNDKELPE
                                                                                                                                                                                                                                                                              Sequence 27559, Application US/09252991A Patent No. 6551795
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                                                                                                                              ILHYVNAANVEINEFSKQVTDWE
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US-09-252-991A-27559
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR PILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-02-18 PRIOR SEQ ID NOS: 33142 SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                        360 EAGLDGIENKLEVPEPVNQNIYEMNREEREAVGIQDLPSTLYTALKAMRENKSIKNALGN 419
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                                                                                                                                                                                                                                                300 IVNSYKRLVPGYEAPCYIAWSGKNRSPLVRVPTSRGLSTRIEVRSVDPAANPYMALAAIL 359
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                                                     KLSSTALGNACHIHMSLODAETEKNAFYDONDEYGMSTLARNWIAGLLKYVPEATYFFAS
                                                                                                                                              242 KPLFGVNGSGMHFNVSL--FKGKENAFFDPEGDLQLTDTAYQFTAGVLKNARGFTAVCNP
                            189 NKLEEAGILMEATHPEFLPSQHELNFVPADPLTMADRHIIAKHGVREMAEQSGMVATFMA
                                                                                                                                                                                                      309 YINSYKRLOPLTFAPTKCCWAIDNRTSAFRLCNSKSEGINVELRIGGADLNPYLAFSAII
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132; Conserv
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Best Local S:
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APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-011-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                EGIAGGGYEISSVDTGYSDCHLCADLNSLHLLPWS-EGAVLAISNPHNFVTSEPLFCSPR 119
                                                                                                                                                                                                                                                                          207 RQSFSIDAANBFDPLFEDMYDWCEAQGLDLDTLIHEEGTAQMBINFRHGDALDLADQILV 266
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                                                                                                                                                                                                                                                                                                                                                                                                                               HOWMNISASSGIETFMRSVRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTMADRHII 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKHGVREMAEQSGWVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLA 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNWIAGLLKYVPEATYFFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCNSKSEGIN 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VELRIGGADLNPYLAFSAIIAAGISGIEEKLELPPPASGNVYNDKELPEFPNSLONATHL 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MIITYDELNNLIRNGKIDTVVLACVDMQGRLMGKRLTGRHFLGLDQKKISISTFVYAVTI 60
                                                                                                                                                                                      267 FKRTMREAALKHNVAATFMAKPMTGEPGSAMHLHQSIVDVKTGKNIF--SNADGTMSELF
                                                                                                                  Gaps
                                                                                                                26;
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                                                                 ; Score 450; DB 4; Length 48; Pred. No. 7.3e-41; 80; Mismatches 222; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             409 LKESKMLNKTFGEKLILHYVNAANVEINEFSKOVTDWE 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          444 MENCKPLEQYLGSKFISGYVAVKRAEHENFKRVISSWE 481
                                                                                                                                                                                                                                                                                                                                      120 VILMQQIERLANLKLKGLFASELEFNLFNET--
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Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4173
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27833
                                                               18.9%;
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Best Local Similarity 28.2%
Matches 111; Conservative
                                                                                                             Matches 130; Conservative
                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-134-001C-4173
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LENGTH: 452
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ORGANISM:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC99-03PA
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APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

IITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE. REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-7

NUMBER OF SEQ ID NOS: 33142
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LOCATION: (769)
OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----EDGSGCRYEPRNILKKLLNQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 DEVEKAALLQSIEITAIVAESSPGGYELNLQHNHDILKLCDQINALKRIVKQVARKHDLT 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       364 FSAIIAAGISGIEEKLELPPPASGNVYNDKELPEFP-----NSLQNATHLLKESKMLN 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394 TATILAGASYGLSHKLPLPKPA------HLLKPPDEHILLANNQPEALKIFKGSLILK 445
                                                                                                                                                                                                                                                                                                                                                                                                            68 DINGHIRGKRIDVKSL----KNLSNGCYFPLSVYAMSLDGKVIEETGLGKYIGEPDRLC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 ATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLARNWIAGLLKYVPEAT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 YFFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCNSKSEGINVELRIGGADLNPYLA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 LHANNYFPVMAAELEFYLFSPQHQS-----BICSBNQCFDIDAPNNYQ----QVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 -----GYSDCHLCADLNSLHLLPWSEGAVLAISNPHNFVTSEPLFC--SPRVILMQQIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LANLKLKGLFASELEFNLFNETYKSASOKHWKNLKTAOPHHQWMNISASSGIETFMRSVR
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                                                                                                                                                                                                                                                                                                                                                                  26 DMQGRLMGKRLTGRHFLGLDQKKISISTF----VYAVTIEG----IAGGGYEISSVDT--
                                                                                                                                                                                                                                                                                                                      75;
                                                                                                                                                                                                                                                                            Length 480;
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                                                                                                                                                                                                                                                                            Query Match 14.0%; Score 331.5; DB 4; Best Local Similarity 25.7%; Pred. No. 1.1e-27; Matches 117; Conservative 76; Mismatches 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417 KTFGEKLILHYVNAANVEINEFSKOVTD----WEL 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: GTC99-03PA
CURRENT PFLING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 LPILGSLOPSALSPELNAQLYLSMQE-
                                                                                                                                                                                             ; ORGANISM: Acinetobacter baumannii
US-09-328-352-6949
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US-09-252-991A-16796
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                                                                                                                                          SEQ ID NO 6949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 TGLVWDVGDADCWTFPLPGSLTLQPWRQSPTGQVQVSMHPELGLPAAA--GDPRHVLQRV 163
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                                                                                                     469 OMGIETLPRTLSEAIDAFEADPLSRQVFGDAMYQAFVEFKRDEWNAYHTHVSDWEIQR 526
                                                                            ---LPEFPNSLQNATHLLKESKMLNKTFGEKLILHYVNAANVEINEFSKQVTDWELNQ 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 IHSLQAEGFHPVMAVELEFYLLDRERDSDGRPLPALQMNGQRPRATQVY----GVYELEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IETFMRSVRNKLEEAGILMEATHPEFLPSQHELNFVPA-DPLTMADRHIIAKHGVREMAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 LIRNGKIDTVVLACVDMQGRLMGKRLTGRHFLGLDQKKISISTFVYAVTIEGIAGGGYEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299 VPEATYFFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCNSKSEGINVELRIGGADL
                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATI
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196:136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PELLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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26.8%; Pred. No. 4e-29;
tive 73; Mismatches 231;
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                                                                                                                                                                                                                                Sequence 19014, Application US/09252991A Patent No. 6551795
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Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
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Matches 122; Conserv
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TITE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136 CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR PFLICATION NUMBER: US 60/074,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 32811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---MOQIER----LAN-----LKLKGL-----FASELEFNLFNET-YKS------A 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 32811, Application US/09252991A; Patent No. 6551795; GENERAL INFORMATION:
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Matches 119; Conservative
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US-09-252-991A-32811
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US, 60/03/25, 991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US, 60/094,190
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
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                                                                    Length 1037;
                                                             ; Score 317; DB 4; Length 10; Pred. No. 1.7e-25; 67; Mismatches 200; Indels
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                                                         Query Match
Best Local Similarity 27.34
Matches 113; Conservative
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Matches 99; Conservative
US-09-252-991A-16796
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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272 KNAFYDQNDEYGMSTLARNWIAGLLKYVPEATYFFASYINSYKRLQPLTFAPTKCCWAID 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 NRTSAFRLCNSKSEGINVELRIGGADLNPYLAFSAIIAAGISGIEERLELPPPASGNVY- 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         391 NDKE-----LPEFPNSLQNATHLLKESKMLNKTFGEKLILHYVNAANVEINEFSKQVTD 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
10.2%; Score 241.5; DB 4;
Best Local Similarity 29.5%; Pred. No. 2.1e-18;
Matches 56; Conservative 38; Mismatches 89:
                  SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
APPLICATION NUMBER: US/09/107,532A
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: 1314 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-8277
INFORMATION FOR SEQ ID NO: 4613:
SEQUENCE CHARACTERICICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature;
;
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LOCATION: (B) LOCATION 1...190
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;
SEQUENCE DESCRIPTION: SEQ ID NO: 4613:
US-09-107-532A-4613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6200, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: «Unknown»
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEI
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 190 amino acids TYPE: amino acid
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STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445 WELNQGFNRY 454
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US-09-107-532A-6200
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                                                                                                                     Sequence 4363, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 DPFFAREPTVVVTCDVIEPSTGQGYERDPRSIARRAEEYLKSTGIGDTAFFGPEPEFFVFD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----YKSASQKHWKNLK------TAQPHHQWMN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 EVKWDIDMSGARHTLIAEEAAWSTGKDYESGNSGHRPRVKGGYFPVPPVDSAQD----MR 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 REMAEQSGMVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEY-GMSTLARNWI 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIGGADLNPYLAFSAIIAAGISGIEEKLELPPPASGNVYN-----DKELPEFPNSLONAT 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 ISASSGIETFMRSVRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTMADRHIIAKHGV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 AGLLKYVPEATYFFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRL-CNSKSEGINVEL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 GGIIKHARALNAITNPSTNSYKRLVPHFEAPIMLAYSARNRSASIRIPYVSNPKGKRIEA 379
  398 AADKNLYDLPPEEAKEIPQVCGSLKEALEELDKGRAFLTKGGVFTDEFIDAYIELKSEE 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 EPLFCSPRVILM------QQIERLANLKLK-----GLFASELEFNLFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 AEMCAKIEDIMGPGR-----VEVHHHEVASCQLEIGVSFNTLVRKADEVQQFKYAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 489;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.8%; Score 255.5; DB 4; 24.7%; Pred. No. 3.1e-19; ive 57; Mismatches 156;
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MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4613, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Acinetobacter baumannii
US-09-328-352-4363
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STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 24.7<sup>7</sup>
Matches 98; Conservative
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                                                                           RESULT 12
US-09-328-352-4363
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LENGTH: 489
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DB 4; Length 481;

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82 LCADLNSLHLLPWSEGAVLAISNPHNFVTSEPLFCSPRVILMQQIERLANLKLKG--LFA 139
                                                                                                                                                           81 LCANLNLIFKKEMFEAHIHELEALMNGKTH---FSSTTINYTLSGKRI-DVQLRGAILPG 136
                                                                                                                                                                                                                                                                                                                                                     285 ----STLARNWIAGLLKYVPE----ATYFFASYINSYKRLQPLTFAPTKCCWAIDN--R 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 SELEFNLFNET-----YKSASQKHWKNLKTAQ-----PHHQWMNISASSGIETFMRSV 187
                                                                                                                                                                                                                                                                       137 SETTFDRILITTEDITPYQNALRQEEKNRRLAESMFIYSPTSLW------VEDFSR-I 187
                                                                                                                                                                                                                                                                                                                       188 RNKLEEAGIL------MEATHPEFLPSQHE-----LNFVPADPLTMADRHIIAKHGVR 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 IFAEE--MVETFREQLIELWQGNIHHKREAVNYALDGQIRNVLLQFTVFPGYEETWGLVQ 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334 TSAFRICNSKSEGINVELRIGGADINPYLAFSAIIAAGISGIEEKLELPPPASGNVY--- 390
                                                                                                                                                                                                                                                                                                                                                                                                                  235 EMAEQSGMVATFMAKLSSTALGNACH-----IHMSLQDAETEKNAFYDQNDEYGM-- 284
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                              4.0%; Score 95; DB 4; Length 481.
20.0%; Pred. No. 0.21;
Live 69; Mismatches 170; Indels
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Job time: 22 secs
                              Query Match
Best Local Similarity 20.09
Matches 84; Conservative
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03P-08
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 ITGEEIKRIIEEENVRFLRLMFTDILGTIKAVEVPVSQIDKVLENKAMPD----GSSIEG 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.6%; Score 134; DB 4; Length 275; Best Local Similarity 23.0%; Pred. No. 3.6e-06; Matches 63; Conservative 33; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 PADPLTMADRHIIAKHGVREMAEQSGMVATFMAK 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILLING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...275
SEQUENCE DESCRIPTION: SEQ ID NO: 6200:
                                                                                                                                                                                                                                         NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                   APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998 APPLICATION NUMBER: 60/051571 FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4580, Application US/09328352
Patent No. 6562958
                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 6200:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-107-532A-6200
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LENGTH: 481
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December 17, 2003, 22:37:15 ; Search time 39 Seconds (without alignments) 1847.740 Million cell updates/sec
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/gcgdata/geneseg/genesegp-emb1/AA2002.DAT;
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/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:'
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SOMMAKIES	
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Result		Query				
No.	Score	Match	Match Length DB ID	DB	ID	Description
-	614.5	25.9	459	22	AAG80030	Pseudomonas as KIE
8	614.5	25.9	459	22	AAG80038	Pseudomonas putida
m	502.5			22	AAU54831	Propionibacterium
4	475.5			23	ABP53500	Brevibacterium lac
'n	470.5			22	AAG92188	C glutamicum prote
9	470.5		1 446	22	AAB79681	Corynebacterium gl
7	464			23	ABB55555	Lactococcus lactis
80	453			23		Bifidobacterium lo
6	445			23		Streptococcus poly

treptococcus treptococcus		Staphylococcus aur	Staphylococcus aur	Staphylococcus aur	Listeria monocytog	S. epidermidis ope	Staphylococcus epi	Enterococcus faeca	Peptide with gluta	Mycobacterium tube	Putative P. abyssi	Herbicidally activ	C glutamicum prote	Corynebacterium gl	Mycobacterium tube	Bifidobacterium lo	Mycobacterium tube	Mycobacterium tube	Propionibacterium	Haemophilus influe	Novel human diagno	S. murayamaensis A	Pseudomonas aerugi	icobacter	N. gonorrhoeae ami	Salmonella typhi c	' E. coli cellular p	human	el human	eumoni	Novel human enzyme	Human ORF1611 prot	LACING OPEY OPE1241
ABP27863 AAU37785	AAE33506		AAU36745	AAU37182	ABB48084	AAG82578	ABP39328	AAU34921	AAP93191	AAW37905	AAB96475	ABB92646	AAG93231	AAB79682	AAW18160	ABP65893	AAW63035	AAW37901	AAU54574	AAU35544	ABG24868	ABP57636	AAU36495	AAU35914	ABP80864	AAU38196	AAU34825	ABG13707	ABG25229	AAY85879	œ	ABP32638	AAR41477
	24	5 7 7	22	22	23	22	23	22	10	19	22	23	22	22	18	23	13	13	22	22	22	24	22	22	24	22		22	22	19	22	23	21
44 448	448	446	446	446	444	446	452	451	443	446	483	845	477	477	478	478	478	478	533	472	1038	200	469	481	524	469	469	816	476	185	334	118	159
	18.2			•	•	•	٠	16.9	16.9			14.0		13.6	12.9			12.8	12.4	12.1	12.1	11.8	11.2	11.2	10.8	10.4	10.1	9.1	•	•	7.1	6.8	6.2
441	432	424.5	24.	424.5	410	409	409	402	400.5	393.5	389.5	333	322	322	306	305.5	303	303	294.5	287	287	281.5	265.5	265	255.5	247	241	16	201.5	8	169.5	160.5	147.5
10	12	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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L-alaninol; isopropylamine; iupI; ipuH; ofloxacin; ipuC; glutamylamide; gamma-glutamylamide synthase; theanine.
                                                                                                                                                                                                                    De Azevedo Waesch SI;
                                                                                                                                                                                                                      Kiener AM,
                                                             Pseudomonas sp KIE171-BII ipuC protein.
        AAG80030 standard; Protein; 459 AA.
                                                                                                                                                                                                                    Leisinger T, Van Der Ploeg J,
Maire T;
                                                                                                                                                                30-MAR-2001; 2001WO-EP03651.
                                                                                                                                                                                  31-MAR-2000; 2000EP-0106888
                                            (first entry)
                                                                                                                                                                                                                                               WPI; 2001-626266/72.
N-PSDB; AAI68686.
                                                                                                                                                                                                  (LONZ ) LONZA AG.
                                                                                                                            WO200173038-A2.
                                                                                                           Pseudomonas sp.
                                            17-JAN-2002
                                                                                                                                              04-OCT-2001.
                          AAG80030;
AAG80030
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New microorganism for converting isopropylamine to L-alaninol, useful

De Azevedo Waesch SI;

Kiener AM,

Van Der Ploeg J,

Leisinger T,

Maire T;

(LONZ) LONZA AG

WPI; 2001-626266/72.

N-PSDB; AAI68692

30-MAR-2001; 2001WO-EP03651 31-MAR-2000; 2000EP-0106888

WO200173038-A2

04-OCT-2001

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This invention describes novel microorganisms (A), or their enzymatic extracts, able to convert isoproplamine (I) to L-alaninol (II) and which have the ipuH and ipuI genes, encoding enzymes involved in metabolism of (II), inactivated. (II) is an intermediate for pharmaceuticals, especially ofloxacin. Also the enzyme encoded by the bacterial ipuC gene (a gamma-glutamylamides, sprthase) is used for synthesis of gamma-glutamylamides, specifically theanine. Inactivation of the ipuH and I genes were inactivated produced (II) at 8 mm after 60 hour culture. For a shmilar strain in which only the ipuI had been inactivated the maximum (II) concentration was about 7 mM, after 6 hour, falling to practically zero after about 20 hour. This sequence represents the Pseudomonas putida KIEI/I-BII IpuC protein products (potential glutamine synthetase) which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGGYEISSVDTGYSDCHLCADLNSLHLLPWSEGAVLAISNPHNFVTSEPLFCSPRVILM 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182
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 ofloxacin, has the ipuH and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 ELNNLIRNGKIDTVVLACVDMQGRLMGKRLTGRHFL---GLDQKKISISTFVYAVTIEGI
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                                                                                                                                                                                                                                                                                                                                                                                                               25.9%; Score 614.5; DB 22;
ilarity 34.8%; Pred. No. 5e-51;
Conservative 73; Mismatches 194;
as pharmaceutical intermediate especially genes for alaninol catabolism inactivated
                                                        German.
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                                                        Example 1; Page 93-94; 106pp;
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Matches 159; Conserv
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This invention describes novel microorganisms (A), or their enzymatic extracts, able to convert isopropylamine (I) to L-alaninol (II) and which have the ipuH and ipuI genes, encoding enzymes involved in metabolism of (II), inactivated. (II) is an intermediate for pharmaceuticals, especially ofloxacin. Also the enzyme encoded by the bacterial ipuC gene (a gamma-qlutamylamides ynthase) is used for synthesis of gamma-glutamylamides specifically theanine. Inactivation of the ipuH and I genes improves production of (II). Typically, a Pseudomonas in which both ipuH and I genes were inactivated produced (II) at 8 mM after 60 hour culture. For a similar strain in which only the ipuI had been inactivated the maximum (II) concentration was about 7 mM, after 6 hour, falling to practically zero after about 20 hour. This sequence represents the pseudomonas putida. IpuC encoded protein described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 --DGLEFTGWDSGYPDIALIPDLSTLSLVPWQEKTASVLCDIQH-LNGEPLNLSPRNLLR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 IAAKHGMTATFMAKPSAEWSGSSGHVHMSLSDLAGTP--VFANPENPGALSEVGYNFLAG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| |||| :| : |: ||| || || : | : || 358 GADTNPYLVIAASLESAAGIFR 415
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                                                                                                                                                                                                                                                                                                                                                 New microorganism for converting isopropylamine to L-alaninol, useful as pharmaceutical intermediate especially ofloxacin, has the ipuH and genes for alaninol catabolism inactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 AGGGYEISSVDTGYSDCHLCADLNSLHLLPWSEGAVLAISNPHNFVTSEPLFCSPRVILM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 MVALAREMSAIYLPNÍNSÝKRTAGASWAGGNSSWGFDNRTVSHRAITSAGSAARVENRIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355 GADLNPYLAFSAIIAAGISGIEEKLELPPPASGNVYNDKELPEFPN----SLQNATHLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----HHOMMIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 KAIEKAEQLGYKCYAAYEFEFYLLNDSIASISADQWRSINPVEKSGHCYSMLHH-----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASSGIETFMRSVRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTMADRHIIAKHGVRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 MAEQSGMVATFMAKLSSTALGNACHIHMSLQD-AETEKNAFYDQNDEYGMSTLARNWIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 ELNNLIRNGKIDTVVLACVDMQGRLMGKRLTGRHFL---GLDQKKISISTFVYAVTIEGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 QOIERLANLKLKGLFASELEFNLFNETYKSASOKHWKNLKTAOP----
                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Fig 3A-N; 106pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     459 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                character and the proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused in P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central enrouses system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies pepcific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent directly from WIPO and polyperides in the printed format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                   SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endopthealmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 21.1%; Score 502.5; DB 22; Length 472; Best Local Similarity 32.1%; Pred. No. 4.9e-40; Matches 135; Conservative 81; Mismatches 169; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bhatia A;
Propionibacterium acnes immunogenic protein #15727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitcham JL, Wang SS,
Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID No 16026; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                          AAU54831 standard; Protein; 472 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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L'maisonneuve J, Zhang Y,
                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                             Propionibacterium acnes
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                                                                                                                                                                                                                                                                                                                                                                                WO200181581-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brevibacterium lactofermentum; glnA2; glnE; L-glutamine; fermentation; coryneform bacterium; glutamine synthetase adenylyl transferase; glutamine synthetase; liver function promoting agent; enzyme; seasoning.
                                                                             170 GESPVALDNGGYFDHTTLGAGTDFRRDAINVLEQMGISVEFSHHEAAPGQHEIDLRYADA
                                                                                                                                                                                                                       348 PMYKPDKASSARVELRSIDSAANPYLAYSLVLAAGLDGIEKELPLPEEASDDVWQLSARE
                                                                                                                                                                                                                                                                                                                                                                                                                                          408 RHALGIKQLPOSLGAAIRCMESSELVAETLGEHVYDYFLRNKRAEFEEYNROVSOFELDR
                                                    -- ISNPHNFVTSEPLFCSPRVILMQQIERLANLKLKGLFASELEFNLFNETYKSASQKHW
                                                                                                                            160 KNLKTAQPHHQWMNISASSGIETFMRSVRNKLEEAGILMEATHPEFLPSQHELNFVPADP
                                                                                                                                                                                                LTMADRHIIAKHGVREMAEQSGMVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQN
                                                                                                                                                                                                                                                                          DEYGMSTLARNWIAGLLKYVPEATYFFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRL
                                                                                                                                                                                                                                                                                                                                               --- CNSKSEGINVELRIGGADLNPYLAFSAIIAAGISGIEEKLELPPPASGNVY--NDKE
                                                                                                                                                                                                                                                                                                                                                                                                                       ----LPEFPNSLQNATHLLKESKMLNKTFGEKLILHYVNAANVEINEFSKQVTDWELNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coryneform bacterium which has L-glutamine producing ability and has been modified so that its intracellular glutamine synthetase activity should be enhanced, useful for producing L-glutamine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brevibacterium lactofermentum glnA2 protein SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim, 10, Page 26-27; 39pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-629685/68.
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Kurahashi O;
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52 STFVYAVTIEG--IAGGGYEISSVDTGY----SDCHLCADLNSLHLLPWSEGAVLA--- 101

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L-glutamine, by culturing a bacterium in a medium to produce and accumulate L-glutamine in the medium and collecting the L-glutamine. L-glutamine produced by (1) is useful industrially as an ingredient of seasonings, as liver function promoting agents, in amino acid transfusions, and in comprehensive amino acid preparation. (II) is useful for breeding (I). The by-production of L-glutamic acid is suppressed and the production efficiency of L-glutamine is improved using (II). The present sequence represents Brevibacterium lactofermentum glnA2, which has glutamine synthetase activity.
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LAFSVMLGAGLKGIKEGYELDEPAEDDISNLSFRERRAMGYND----LPNSLDQALRQM 402
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                                                                                                                                                                                          GKIDTVVLACVDMQGRLMGKRLTGRHFLGLDQKKISISTFVYAVTIEGIAGGGYEISSVD
                                                                                                                                                                                                       TGYSDCHLCADLNSLHLLPWSEG-AVLAISNPHNFVT---SEPLFCSPRVILMOQIERLA
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                                                                                                                                                                                                                                                                                    NLKLKGLFASELEFNLFNETYKSASQKHWKNLKT-----AQPHHQWMNISASSGIETFM
                                                                                                                                                                                                                                                                                                          DEGLICMISPEIEFYLV-------QSLRINGLPPVPTDNGGYFDQAIFNEAPNFR
                                                                                                                                                                                                                                                                                                                                                 TFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLARNWIAGLLKYVPEATY
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                                                                                                                                                                                                                                                                                                                                                                                                                             FFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCN---SKSEGINVELRIGGADLNPY
                                                                                                                                                                    Gaps
                                                                                                                                                                  71;
                                                                                                                                          20.0%; Score 475.5; DB 23; Length 446; 29.2%; Pred. No. 2e-37; ive 83; Mismatches 174; Indels 71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid synthesis; vitamin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glutamicum protein fragment SEQ ID NO: 5942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAFSAIIAAGISGIEEKLELPPPASGNV---
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2000JP-0159162.
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                                                                                                                                                       Best Local Similarity 29.23
Matches 135, Conservative
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sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, coryneform bacterium, coryneform bacterium, coryneform bacterium coryneform bacterium coryneform bacterium of a gene derived from coryneform bacterium. Coryneform bacterium of a gene derived amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLKLKGLFASELEFNLFNETYKSASQKHWKNLKT-----AQPHHQWMNISASSGIETFM 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | : | : | : | : | : | DEGLTCMISPEIEFYLV -----QSLRINGLPPVPTDNGGYFDQATFNEAPNFR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLARNWIAGLLKYVPEATY 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 VINOWVNSYKRIVYGNEAPTAATWGVSNRSALVRVPTYRLNKEESRRVEVRLPDTACNPY 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAFSAIIAAGISGIEEKLELPPPASGNV------YNDKELPEFPNSLQNATHLL 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
                                                                                                                                                                                                Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKIDTVVLACVDMQGRLMGKRLTGRHFLGLDQKKISISTFVYAVTIEGIAGGGYEISSVD
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                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of nucleotide and protein
                                               Yokoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71;
                                                                                                                                                                                                                                                                                                                             Claim 17; SEQ ID NO: 5942; 246pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 470.5; DB 22; Length
Pred. No. 6.1e-37;
4; Mismatches 174; Indels
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                                               Ochiai
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                                               Σ
                                            S, Hayashi
Ozaki A;
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                                               H, Ando
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84;
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KYOW ) KYOWA HAKKO KOGYO KK
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                                               Mizoguchi
Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Patent Office
                                                                                                                         2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         446 AA
                                                                                                                      WPI; 2001-376931/
N-PSDB; AAH67407
                                               s, z
                                               Nakagawa
Tateishi
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LAFSAIIAAGISGIEEKLELPPPASGNV------YNDKELPEFPNSLQNATHLL 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 TEMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLARNWIAGLLKYVPEATY 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 FFASYINSYKRLOPLTFAPTKCCWAIDNRTSAFRLCN---SKSEGINVELRIGGADLNPY 361
                                                                                                                                                                                                                                                                                                                           AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SFMPKPPQEHAGSANHTHMSLFEGDT--NAFHDPDDSYMLSKTAKQFIAGILHHAPEFTA
                                                                                                                                                                                                              Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purine and pyrimidine bases -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------GSAIEGYA----RISEAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 446;
                                                                                                                                Haberhauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.8%; Score 470.5; DB 22; Length 28.9%; Pred. No. 6.1e-37; Live 84; Mismatches 174; Indels
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                                                                                                                                Zelder
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                                                                                                                                                                                                                                                                                             Claim 20; Page 300-301; 1737pp; English.
                                                                                                                                Schroeder H,
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                  03-SEP-1999; 99DE-1042095.
03-SEP-1999; 99DE-1042124.
03-SEP-1999; 99DE-1042129.
09-MAR-2000; 2000US-0187970.
   99DE-1042088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                Kroeger B,
                                                                                                                                                                WPI; 2001-137957/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                446 AA;
                                                                                                                                                                                 N-PSDB; AAF71800.
                                                                                               BADI ) BASF AG.
                                                                                                                                Pompejus M,
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Matches 134;
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                                                                                                              fine chemical production, microorganism, organic acid, nucleoside,
nonproteinogenic amino acid, purine base, pyrimidine base, nucleotide,
lipid, saturated fatty acid, unsaturated fatty acid, diol, vitamin,
                                                                                                                                                              carbohydrate; aromatic compound; cofactor; polyketide; enzyme
                                                               Corynebacterium glutamicum MP protein sequence SEQ ID NO:96.
                                                                                               Corynebacterium glutamicum; metabolic pathway protein; MP
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99DE-1032206.
99DE-1032227.
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99DE-1031634
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99DE-1032125
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99DE-1040764
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99DE-1042087
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                                                                                                                                                                                             Corynebacterium glutamicum
                                (first entry)
                                                                                                                                                                                                                             WO200100843-A2
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                                30-APR-2001
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AAB79681;
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403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLFCSPRVILMQQIERLANLKLKGL-FASELEFNLF--NETYKSASQKHWKNLKTAQPHH 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QWMNISASSGIETFMRSVRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTMADRHIIA 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                             The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53100-ABB55621). The nucleic acid sequence; is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-O7-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MILIYDELNNLIRNGKIDTVVLACVDMQGRLMGKRL--TGRHFLGLDQKKISISTFVYAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIEGIAGGYEISSVDTGYSDCHLCADLNSLHLLPWSE-----GAVLAISNPHNFVTSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELRIGGADLNPYLAFSAIIAAGISGIEEKLELPPPASGNVY--NDKE----LPEFPNSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KHGVREMAEQSGMVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SFIAGLLKHAYNFTAITNPTVNSYKRLVPGYEAPVYVAWAGRNRSPLIRVPASRGLSTRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MTITAADIRRDVKEKDÍKFLRLMFTDILGTLKNVEVPATDEQLDKLFENKMMFD----GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 PFAGDPRGVLKRNLKSMEKLGFKSFNLGPEPFFFFFKLNENDEPTLEVNDKG-----
                                                                                                                                                                                                                                                                                                                                        useful in the identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
                                                            bacterium; yogurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 23; Length 446;
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                                                                                                                                                                                                                                                                              Ehrlich SD
                                                                                                                                                                                                                                                                                                                                                                                       6; SEQ ID No 2257; 2504pp; French.
                                                                                                                                                                                                                                                (INRG ) INRA INST NAT RECH AGRONOMIQUE
                                                           Biosynthesis; biodegradation; lactic
                                                                                                                                                                                                                                                                              Renault P,
                              Lactococcus lactis protein glnA
                                                                                                                                                                                   11-APR-2000; 2000FR-0004630.
                                                                                                                                                                                                                11-APR-2000; 2000FR-0004630.
                                                                                                                                                                                                                                                                                                                                          New nucleotide sequence use
lactis and related species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 29.0%
Matches 137; Conservative
(first entry)
                                                                                         Lactococcus lactis IL1403
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                                                                                                                                                                                                                                                                             Sorokine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       446 AA;
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16-MAY-2002
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The present invention describes a polynucleotide (I) comprising a sequence of a Bifidobacterium genome selected from the nucleotide acquences given in ABO81842 and ABO81843, or a sequence exhibiting at least 90% identity or which hybridises with the sequence exhibiting at least 90% identity or which hybridises with the sequence given in ABO81842 and ABO81843. Also described is a polynucleotide (II) encoding a heterologous polypeptide in frame to a polynucleotide concoding a heterologous polypeptide. (I) has antidiarrheic and antibacterial activities, and can be used as an inhibitor of Salmonella. (I) (which is a probe) is useful for the detection and/or identification of Bifidobacterium longum in a biological sample. A carrier containing the lactic acid bacterium Bifidobacterium longum NCC2705 (CNCM I-2618) can be used for preventing and/or treating diarrhoea brought about by pathogenic bacteria and/or rotavirus. The carrier is a food composition selected from milk, yogurt, curd, cheese, fermented milks, milk based fermented products, ice-creams, fermented cereal based products, infant formula, pet food or a pharmaceutical composition spelected from tablets, liquid bacterial suspensions, dried oral cupplement, wet oral supplement, dry tube feeding or wet tube feeding. (I) is useful in DNA arrays or chips to carry out analysis of the stidobacterium related nucleotide sequences given in the Sequence infant the present invention but not mentioned further within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N.B. The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bifidobacterium longum NCC2705; Bifidobacterium; bacterial; antidiarrheic; antibacterial; inhibitor of Salmonalla; detection; identification; lactic acid bacterium; diarrhoea; pathogenic bacteria; rotavirus; food composition; pharmaceutical composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotide comprising Bifidobacterium genome sequence useful as a probe or primer for detecting and/or identifying Bifidobacterium
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454
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                                             HNAVKALPEDTIVTEALGEHVLVNFVEAKRIEWASYAQFVSQWEIDNYLELY
QNATHLLKESKMLNKTFGEKLILHYVNAANVEINEFSKQVTDWELNQGFNRY
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                                                                                                                                                                                                                                                                                  ABP66039 standard; Protein; 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as a probe or primer for detec
longum in a biological sample
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Best Local Similarity 31.11
Matches 127; Conservative
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Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
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                                                                                                                                                                                                                                                                                                                      231 HGVREMAEQSGNVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLARN 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :| | | : | | : | | | | : | | : | | | : | : | | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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                                                                                                                                                      FCSPRVILMQQIERLANLKLKGL---FASELEFNLFNETYKSASQKHWKNLKTAQPHHQW 171
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                                                               ---AVLAISNPHNFVTSEPL
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24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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(GENO-) INST GENOMIC RES.
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CC the specification. The proteins have antibacterial and antiinflammatory activity. (1), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.

CN absorbed and an ample. (I) is used to determine whether a compound binds to biological sample. (I) is used to determine whether a compound binds to complete a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be maningitis. Nucleic cused as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be maningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
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Matches 131
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antiblocius, the essential genes themselves and the discovery of novel antiblocius, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part
RLELRSVDPTANPYLALAVLLEAGLDGIINKIEAPEPVEANIYTMTMEERNEAGIIDLPS 394
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                                                SLONATHLLKESKMLNKTFGEKLILHYVNAANVEINEFSKQVTDWELNQGFNRY
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                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae cellular proliferation protein #214.
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Pred. No. 3.7e-33;
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Xu HH;
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23-MAY-2000; 2000US-20684BP.
23-MAY-2000; 2000US-20737P.
23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-255625P.
22-DBC-2000; 2000US-253625P.
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27.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae.
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Yamamoto RT,
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  335
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                                                                                                                                                                                                                                                                                                                                                                                                New Streptococcus protein for the treatment or prevention of infectic or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
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18.6%; Score 441; DB 23; Length 448;
Best Local Similarity 27.4%; Pred. No. 4.8e-34;
Matches 130; Conservative 82; Mismatches 216; Indels 4
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                                                                                        27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                29-OCT-2001; 2001WO-GB04789.
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N-PSDB; ABN68494.
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Claim 7; Page 38; 43pp; English.
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                                                                                                                                                                                                             GPPRGNLKRALRHMEEVGFKSFNLGPEFFLFKLDENGDPTLEVNDKG-----GYF 158
                                                                                                                                                                                                                                                                                                                                     VREMAEQSGMVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGM--STLARN 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanniffy SB;
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                                                                     MPITAADIRREVKEKNVTFIRLMFSDILGTMKNVEIP----ATDEQLDKVLSNKVMFDG
                                                                                                          58 VTIEGIAGGGYEISSVDTGYSDCHLCADLNSLHLLPWSE--GAVLAISNPHNFVTSEPLF
                                                                                                                                                                                   CSPRVILMQQIERLANLKLKGL-FASELEFNLF--NETYKSASQKHWKNLKTAQPHHQWM
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                                                                                                                                                                                                                                                                                  WIAGLLKYVPEATYFFASYINSYKRLOPLTFAPTKCCWAIDNRTSAFRLCNSKSEGINVE
 Gaps
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220;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Encoded by GTTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae ID-216 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein; 448
83;
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Conservative
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128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 CSPRVILMQQIERLANLKLKGL-FASELEFNLF--NETYKSASQKHWKNLKTAQPHHQWM 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 SSIEGF-----VRINESDMYLYPDLDTWTVFPWGDENGSVAGLICDVYTTEGEPFA 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MTITYDELNNLIRNGKIDTVVLACVDMQGRLMGKRLTGRHFLGLDQ---KKISISTFVYA 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 GDPRGNLKRALRHMEEVGFKSFNLGPEPEFFLFKLDENGDPTLEVNDKG-----GYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 448;
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protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
relates to Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 18.2%; Score 432; DB 24; Local Similarity 27.2%; Pred. No. 3.7e-33; Nes 128; Conservative 83; Mismatches 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae type 4 strain.
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159 DLAPTDLADNTRREIVNVLTKMGFEVEASHHEVAVGQHEIDFKYDEVLRACDKIQIFKLV 218
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2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
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                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus.
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N-PSDB; AAS52096.
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26-MAY-2000;
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Yamamoto RT,
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                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae type deminiate UNA coculiy septions from the ABS56454. Also included are an antibody which binds one of the Corpotations, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprision first and second primers, which are the nucleic acid cited above or fragments between nucleotides of a sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target compound the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers complement of the target sequence, and where the parts of the primers of the target sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more contacting the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis media or ear infection. They are also useful for the proteins, the present sequence is one of identifying immunodominat proteins. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                  The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer redable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 VTIEGIAGGGYEISSVDTGYSDCHLCADLNSLHLLPWSE--GAVLAISNPHNFVTSEPLF 115
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                                                                                                                                                                                                                       New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or ear infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 GDPRGNLKRALRHMEEVGFKSFNLGPEPEFFLFKLDENGDPTLEVNDKG-----GYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the 2469 proteins expressed by the identified coding regions from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the printed specification, but was obtained in electronic mat directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.2%; Score 432; DB 24; Length 448; 27.2%; Pred. No. 3.7e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part
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                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 866; 56pp; English.
                                                                                                                                              Fraser C;
                                   27-MAR-2002; 2002WO-IB02163
                                                                  27-MAR-2001; 2001GB-0007658
                                                                                                                                              Masignani V, Tettelin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 128; Conservative
                                                                                               (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
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N-PSDB; ABX06145.
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233 VREMAEQSGMVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGM--STLARN
                                    291 WIAGLLKYVPEATYFFASYINSYKRLOPLTFAPTKCCWAIDNRTSAFRLCNSKSEGINVE
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                        a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at from wipo.int/pub/published_pct_sequences.
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; Pred. No. 2e-32;
92; Mismatches 211; Indels
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, the discovery of novel antibiotics, the essential genes themselves and the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella comential coli, Staphylococcus aureus, Salmonella typhi, Klebsiella comentian is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part

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                                                                                                                                                               Trawick JD,
                                                                                                                                                                                                                                                                                                                                                          New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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Pred. No. 2e-32;
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                                                                                                                                                               Zyskind JW,
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22-DEC-2000; 2000US-257931P.
16-FEB-2001; 2001US-269308P.
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                                                                                                                                                            Ohlsen KL,
Xu HH;
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Search completed: December 17, 2003, 22:42:57 Job time : 43 secs

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A Holygna AP003001 Mesorhizo
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1 WTITYDELNNLIRNGKIDTV......INEFSKQVTDWELNQGFNRY 454
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(c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Perfect score:
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Sinorhizo

AL591790

Description

AE009164 Agrobacte AE008130 Agrobacte AL008883 Mycobacte AE007117 Mycobacte Streptomy

Mycobacte Streptomy

BX248344 R

Pseudomon Pseudomon

Sequence

AX259711

Pseudomon

AE016862

Highly th Thermotog

BD180047 AE004758

AE001758

Streptomy

AF440524 | AP005021 | AP001520 |

Corynebac

DO D

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Sequence Seguence

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AX503498

X60160

T.maritima

Corynebac

AP005281 Corynebac AX127150 Sequence M18966 Clostridium

Pseudomon

Brucella

AE016794 F AE009688 E AE014571 B

Pseudomon

AE016875

AC004396 | AE004467 | AE004630 |

Sequence

AE012342 AE016793 AX492786 S

Brucella

TITLE

COMMENT

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12 (bases 1 to 345783)

S Kaneko, T.

Direct Submission

Institute, The First Laboratory for Plant Gene Research; Yana 1532-3, Kisarazu, Chibaa 292-0812, Japan

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URL: http://www.karusa.or.jp/rhizobase/,

URL: http://www.karusa.or.jp/rhizobase/,

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AIDTLAILSISERELGARNIRVNIVAPGYTHTEMTEGMVGTDFGNMLIAGVPLGQRFGKP
DDIAPTVAFLASDEAAWLTGERINASGGAR"
Mesorhizobium loti DNA, complete genome, section 8/21.
AP003001 BA000012.
AP003001.2 GI:14023393
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/product="short chain 'dehydrogenase or 3-ketoacyl-CoA
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VEUKOUIPPPANLIESMGRYTAERNRRAQILAAGGKQSQILBABGRKBAAFRDAEA
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IVDEVMTRTPKTVDPQTLAGTAIALLNEHNIGALVVTRNNMPLGVVHFHDLLRIGAA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AE014569 11725 bp DNA linear BCT 02-OCT-2002
Brucella suis 1330 chromosome II section 65 of 108 of the complete
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and Fraser, C.M., Hoover, D.L., Lindler, L., Halling, S.M., Boyle, S.M.
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404 AsnAlaThrHisLeuLeuLysGluSerLysMetLeuAsnLysThrPheGlyGluLysLeu 423
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Proc. Natl. Acad. Sci. U.S.A. 99 (20), 13148-13153 (2002)
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Brucella suis 1330
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales;
Brucellaceae; Brucella.
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VERSION
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REFERENCE
AUTHORS
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                                                                                                                                                                                        23 AlaCysValAspMetGlnGlyArgLeuMetGlyLysArgLeuThrGlyArgHisPheLeu
                                                                                                                                                                                                                                                                     GlyLeuAspGlnLysLysIleSerIleSerThrPheValTyrAlaValThrIleGluGly
                                                                                                                                                                                                                                                                                                        GAATCCGGTTATGACGAAACCCACGGCTGCAATTATCTTCTGGCCGACGATATCGATATG
                                                                                                                                                                                                                                                                                                                                            63 IleAlaGlyGlyTyrGluIleSerSerValAspThrGlyTyrSerAspCysHisLeu
                                                                                                                                                                                                                                                                                                                                                                                                                      83 CysAlaAspLeuAsnSerLeuHisLeuLeuProTrpSerGluGlyAlaValLeuAlaIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 ThrHisProGluPheLeuProSerGlnHisGluLeuAsnPheValProAlaAspProLeu
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   169
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2
     Mismatches:
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                                                                              (1-11725)
                                                                            US-10-098-602A-2 (1-454) x AE014569
   43.61%
     Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRERHERKDAAPLTLADCLRLALPGFFIAADLGAWHLSLHSTSVANATLLANMAPIFV
IGAWLLFRSKVSSFYVGLVVAVAQTVUKGGPGELLHSRSSGODAMALLAAVFYAGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MIALITGGIAIGSSPIFVRLSEVGPLATGFWRLALAVLPLLLMD"
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198
82
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note="similar to GP:3236220, and
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Matches:
Conservative:
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61.67%
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Pred. No.:
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Gene name confidence : hypothetical
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1707. .2996

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/note="Product confidence : putative

Gene name confidence : putative

Gene name confidence : hypothetical

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predicted by Homology
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Laboratoire de Biologie Moleculaire des Relations
Laboratoire de Biologie Moleculaire des Relations
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B-5030 Gembloux, Belgium. E-mail:Jerome.Gouzy@toulouse.inra.fr
http://sequence.toulouse.inra.fr/meliloti.html.
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Sinorhizobium meilloti strain 1021
Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9877-9882 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5181
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                                                                                                                                                                                                                                5002 TATCTGGCCTTTGCAGCGCTCATCGCCGGCCTGAAAGGCGTGGAAAAGAGTGGAAAAGTGGAA 5061
                                                                                                                                                                                                                                                                                                                                       381 LeuProProProAlaSerGlyAsnValTyrAsnAspLysGluLeuProGluPheProAsn 400
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                                   341 AsnSerLysSerGluGlyIleAsnValGluLeuArgileGlyGlyAlaAspLeuAsnPro
                                                                              TyrLeuAlaPheSerAlaIleIleAlaAlaGlyIleSerGlyIleGluGluLysLeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                                  5062 CTGGACGAACCTTTTGTGGGCGATGCCTATAGCGCGGTGAGGCTGAAGGAAATTCCTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5122 ACGCTGCGCGAGGCGGCTGCGGCTCAAAGGTTCCGCTTTCCTGAAAGAAGCCTTCGGC
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Sinorhizobium meliloti
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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/mol_type="genomic DNA"
/strain="1021"
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155. .1519
/gene="SMc01575"
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AL591790.1 GI:15075230
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7979
  AGYRLCGEGSKAIRIECRVGGSDLNPYLAFAALIAAGIAGIENKMELEAPFVGDAYQG
KEVREIPHTLREAGEALSGSKMLRAAFGEEVVDHYVHAAEWEQQEYDRRVTDWEVARG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7858 GAGATGGAGACCGTGCCCGGCTACAAGGCGACGAGGCTGGGAGAAAGGTTACGGCGACTAC 7799
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                                                                                           /gene="SWc01597"
complement(8131...9678)
/gene="SWc01597"
/function="cell processes; transport of small molecules;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8038 ATGAGCTATTCGTTCGAGGAACTGAAAGAGATGTTGCCGCCGGGCGCATCGACACGGTG
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Matches:
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IYNTHHGMTNAVVMPPVLRFNRSAIEEKIGRAAAYLGIAGGFDGFYDYVLRLREELGV
PDKLSALGVGTDRIDEMAEMAIVDPTAGGNPVELTLDAAEKLFAECI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'db_xref="GI:15075235"
'db_xref="SPTREMBL:Q92NJO"
'translation="MTMIRCVSPVDGEVYAERPAIPLEMARQAVAHARLAQKAWARRP
                                                                                                                                                                                                                                                                                                                                                                                                   DLGKCVAFMAGQTRPVWDFEDIGDWWTRASVEGIAPIVAVPTTAGTGSEVGRASVITN
SASHVKKVIFHPKFLPGVTICDPELIVGMPKVITAGTGMDAFAHCLEAYSSPFYHPMS
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KPLVVEESDRFERRIAREPHGVVFVIAPWNYPYMTAINTVAPALMAGNTVILKHASQT
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PRPTEKSVAWSNYKJGNPLDETTLEPRANTRAFAATVRUQVADAISKARRALIDPKL
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                                                                                                                                                                                                                                                                                                                                                            'translation="MTITANWSYPTAVKFGAGRIKELADHCKALGIKKPLLVTDRGLA
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Gene name confidence: hypothetical
predicted by Codon usage
predicted by Homology
predicted by FrameD"
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predicted by Homology
predicted by FrameD"
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complement (3949. .5094)
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PVPGYBAAGWDKGYGDFVMKPDLSTLRLAPWLEKTAIVLCDVLDHHHDDLSHSPRAVL
KKQVQRLHERGYRAYFASELEFYIFDETYKSARAKRWHEMETASPYVQGYVIHLTTRE
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Laboratoire d'Immunologie et de Microbiologie, Universite of Namur,
El rue de Bruxelles, Namur 5000, Belgium
(Dases 1 to 12340)
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                                                                                                                                                                                                                                                                                                                                                                                 Submitted (13-NOV-2001) Faculte de Medecine, INSERM U431, Avenue
Kennedy, Nimes 30900, France
Location/Qualifiers
Estably, A., Reznik, G., Jablonski, L., Larsen, N., D'Souza, M., Bernal, A., Mazur, M., Goltsman, E., Selkov, E., Haselkorn, R., Kyrpides, M. and Overbeek, R. Direct Submission Direct Submission (13-NOV-2001) Integrated Genomics, Inc., 2201 W. C Park Drive, IL 60612, USA E Chassen 1 to 12340)
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                                                                                  281 GluTyrGlyMetSerThrLeuAlaArgAsnTrpIleAlaGlyLeuLeuLysTyrValPro
                                                                                                                 7138 GAGGTCACCTATTTCCTGCGCCCTATATCAACTCCTACAAGCGCTTCATGGCGGTACC
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Brucella melitensis 16M
Brucella melitensis 16M
Brucellaceae; Brucella.

1 (bases 1 to 12340)
DelVecchio, V. G., Kapatral, V., Redkar, R.J., Patra, G., Mujer, C., Los, T., Ivanova, N., Anderson, I., Bhattacharyya, A., Lykidis, A., Reznik, G., Jablonski, L., Larsen, N., D'Souza, M., Bernal, A., Mazur, M., Goltsman, E., Selkov, E., Elzer, P.H., Hagius, S., O'Callaghan, D., Letesson, J.-J., Haselkorn, R., Kyrpides, N. and
                                                                                                                                                                                                                                                                       PheAlaProThrLysCysCysTrpAlaIleAspAsnArgThrSerAlaPheArgLeuCys
                                                                                                                                                                                                                                                                                                                                                                 341 AsnSerLysSerGluGlyIleAsnValGluLeuArglleGlyGlyAlaAspLeuAsnPro
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Brucella melitensis
Proc. Natl. Acad. Sci. U.S.A. 99 (1), 443-448 (2002)
11756688
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Submitted (13-NOV-2001) Institute of Molecular Biology and
Medicine, University of Scranton, Scranton, PA 18510, USA
3 (Dases 1 to 12340)
Elzer, P.H. and Hagius, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (13-NOV-2001) Department of Veterinary Science, I
Center, 111 Dalrymple Building, Baton Rouge, LA 70803, USA
4 (bases 1 to 12340)
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II, section 53
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AE009691 AE008918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 LeuProTrpSerGluGlyAlaValLeuAlaIleSerAsn-----ProHisAsnPheVal 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 HisGluLeuAsnPheValProAlaAspProLeuThrMetAlaAspArgHisIleIleAla 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3398 ATTGGAAAGCGCTTCTACGGACAGTTTTTCGTGGAATCCGGTTATGACGAAACCCACGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 IleArgAsnGlyLysIleAspThrValValLeuAlaCysValAspMetGlnGlyArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 MetGlyLysArgLeuThrGlyArgHisPheLeuGlyLeuAspGlnLysLysIleSerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 SerThrPheValTyrAlaValThrIleGluGlyIleAlaGlyGlyGlyTyrGluIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 SerValAspIhrGlyTyrSerAspCysHisLeuCysAlaAspLeuAsnSerLeuHisLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3278 GGTTGGGACAAAGGCTATGGCGATTTCGTCATGAAGCCGGATCTCTCCACGCTGCGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 ThrSerGluProLeuPheCysSerProArgVallleLeuMetGlnGlnIleGluArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 AlaAsnLeuLysLeuLysGlyLeuPheAlaSerGluLeuGluPheAsnLeuPheAsnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrTyrLysSerAlaSerGlnLysHisTrpLysAsnLeuLysThrAlaGlnProHisHis
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                                  ATPGTRVFADVRGNKVPVDVHALPFTPHRYRKG"
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon start=1
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949.50
61.57%
43.82%
39.96%
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Best Local Similarity:
Query Match:
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Pred. No.:
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DEITDAGTQTAWGRKLTAILKKYQETWRSAGGAYPYA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'tränslation="Metrappisasvaelineridampagersaaqmliadypmlglkt
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DQWLSPIARVARHVLAGRIAVPSAMDSSAALFVLAETIIREMTRMLEKDSAARIAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRVLPWSELVFATGARARIPDVPGVALEGVVTLRRMEDARRIAAMMPDVRNVVIIGGG
FIGLEMAHSAIALGKKTVLIEAAPRVLGRSVAAPVSAHVEARSRAADITLLTGLGVAS
IEGENGRAIGVTAGDGTFFPADLVVIGTGAVPNVELAAKAGLSIDNGIRVDEHMRTSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHVYAIGDCASYAHFHAGRHVRLESVQNATDQAKHFARTIVGRETPYREVAWFWSDQG
DMKLQTAGLSFDADRHVLSGEPEENAFSVFSFQGRQAGGGRFHQSPGRSYDCASSACG
GDQPKRGRYYGWYAAPQGIAGGCGAIKVLWKRPDLGGGEESVRFLIAEGMGGGETPGD
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db_xref="G1:17984731"
translation="MFFLGSRKRMLSRSFHFKGDRLVAVDSINRPADHMIARRLLAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTRDHAGLFDISHMKLVEVSGADAAALLAETCPLDPTILKTGGSKYTFFLNDNGGVLD
DLIVTRLGBENEMVVANGARDADIEHLNEAAGGKAVKVNENDLNEVLALGGFERARVI
TDAGLPGADLAFWSGFEPKGSWFWTRSGYTGEDGFEIGLPADBARALAEKLLADERVE
WIGLAARDSIRLEGGLCLHGQDITPETDPVSAGLTWAITKAVREKAAFNGAKAVLDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'tränslation="MSGNFGGPMDDRCIIIGAGHAGSQAAVSLRQEGYAGEIILINDE
TDIPYHKPPLSKSYLKAPEKGSLVLRPESAYRDNNIEMLPGAHVDAVSIAERTVTLGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="TRANSCRIPTIONAL REGULATOR, RPIR FAMILY"
protein id="AAL53798.1"
db_xref="GI:17984729"
                                                                                                            product="Hypothetical Cytosolic Protein"
protein id="AAL53797.1"
db_xref="GI:17984728"
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protein id="AAL53801.1"
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product="RHODOCOXIN REDUCTASE"
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db_xref="GI:17984730"
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codon start=1
trans[_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                       476. .5318
gene="BMEII0556"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406. .6803
gene="BMEII0557"
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gene="BMEI10556"
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/transl rev
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transl_table=1
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LABEKNVSVLNTAIVERAAYRDIFDYGGTLLCLDCKKVSNIDKAVBATAFAEEVIKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /trānslation="MTARFSLFSSLIAVALLGLPVVVQAASFKELSGQGYKVGALSSN
KAGIRGWNLSKGSDRYFCEMRATMAYSGKNGMVSFTSAGRMISLDRNTVAKGLGGSLD
LPKYEDLKAGRLRADDVGSCRKVT"
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SQTHVKAIIFHPKLLEGVVICDPELIVGMPKVITAGTGMDAFAHCLEAYSSPFFHPMS
                                                                                                                                                                            Wood, D.W., Setubal, J.C., Kaul, R., Monks, D., Chen, L., Wood, G.E., Chen, Y., Woo, L., Kitajima, J.P., Okura, V.K., Almeida Jr., N.F., Zhou, Y., Bovee Sr., D., Chapman, P., Clandenning, J., Deatherage, G., Gillet, W., Grant, C., Guenthner, D., Kutyavin, T., Levy, R., Li, M., McClelland, B., Palmieri, A., Raymond, C., Rouse, G., Baulsen, I., Karp, P., Romero, P., Zhang, S., Yoo, H., Tao, Y., Biddle, P., Jung, M., Krespan, W., Perry, M., Gordon, D., Liao, L., Kim, S., Hendrick, C., Zhaog, Z., Dolan, M., Tingey, S. V., Tomb, J., Gordon, M.P., Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (27-SEP-2001) Department of Microbiology, University of
Washington, 1959 NE Pacific Ave, Box 357242, Seattle, WA
98195-7242, USA
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/note="identified by sequence similarity; putative; ORF
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located using Blastx/Glimmer"
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                              the natural genetic engineer Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Agrobacterium tumefaciens str. C58
Washington)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="putative; ORF located using /codon start=1 /transT_table=11
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protein_id="AAL43127.1"
db_xref="GI:17740601"
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                                                                            Science 294 (5550), 2317-2323 (2001)
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complement(77. .793)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
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complement (77. .793)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (958. .1338)
/gene="Atu2137"
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/gene="Atu2137"
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/transl_table=
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/transl_table=
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                                                 tumefaciens C58
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                                genome of
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JOURNAL
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AUTHORS
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                              TITLE
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Agrobacterium tumefaciens str. C58 (U. Washington)
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae, Rhizobium/Agrobacterium group; Agrobacterium.

E (Dasses 1 to 10069)
S Wood, D.W., Setubal, J.C., Kaul, R., Monks, D., Chen, L., Wood, G.E., Chen, Y., Woo, L., Kitajima, J. P., Okura, V.K., Almeida Jr., N.F., Zhon, Y., Bovee Sr., D., Chapman, P., Clendenning, J., Deatherage, G. Gillet, W., Garat, C., Guenthner, D., Kutyavin, T., Levy, R., Li, M., McClelland, B., Palmieri, A., Raymond, C., Rouse, G., Saenphimmachak, C., Wu, Z., Gordon, D., Eisen, J.A., Paulsen, I., Karp, P., Romero, P., Zhang, S., Yoo, H., Tao, Y., Biddle, P., Unng, M., Kreppan, W., Perry, M., Gordon-Kamm, B., Liao, L., Kim, S., Hendrick, C., Zhao, Z., Dolan, M., Tingey, S.V., Tomb, J., Gordon, M.P., Olson, M.V.
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2867 CAGGAGCTGAACGTGCGTATTGCAAGGCGCTTGAAATGGCCGATCGCCACGTCATCATG 2808
                                                                                                                                                                                                                                              2688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2267 AAAGGTTCCGCTTTCCTGAAAGAAGCCCTTCGGCGAGGATGTCGTGAACCATTACACCCAT 2208
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AE009164 AE008688
AE009164.1 GI:17740599
                                                                                                                LeuSerSerThrAlaLeuGlyAsnAlaCysHisIleHisMetSerLeuGlnAspAlaGlu
                                                                                                                                                                                                                        [||:::||| ||:::|
2747 TATGATTATGCAAGGCTGGCAGTTCGAGCCATGTGCACAATTCCATCTGAAGTGCAGAT
                                                                                                                                                                                                                                                                                                                                IleAsnSerTyrLysArgLeuGlnProLeuThrPheAlaProThrLysCysTrpAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     330 IleAspAsnArgThrSerAlaPheArgLeuCysAsnSerLysSerGluGlyIleAsnVal
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                                                                                                                                                                                                                                                                                                  270 ThrGluLysAsnAlaPheTyrAspGlnAsnAspGluTyrGlyMetSerThrLeuAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                     AsnTrplleAlaGlyLeuLeuLysTyrValProGluAlaThrTyrPhePheAlaSerTyr
                                                                                  LygHisGlyValArgGluMetAlaGluGlnSerGlyMetValAlaThrPheMetAlaLys
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SOURCE
ORGANISM
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VERSION
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AUTHORS
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YSLSRAGYFPTVLSITHSKYRTPYVANITGAIVGLAVMLVIWFSLGAEQGGSIIGSVL
LNMAVFGAMFSYIMQAISFILLRKNIPNIERPFRSPFGIPGALLTIIIAIVTLLYQIQ
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LLGNFREVEIGILHDNDSRLADAMLAGAEGASLTVRRNDPYGFBDGVTHTLRLHALPDG
LLNVMIEIRNDLIANEGEQAAIAGFLHELMGKALSSIEE"
9913. 9791
                                                                                                                                                                                                                                                                 GGFVTGLCENVEYVLTPAVVVTFITAVVNSILGLDPAYSPFVMIVFYAI FLALMVFGL
ELSFKVTLVITLISLAVLVFFWISAIPNIDFSRFALMIGVGPDGKAVELPEGGGGSFFP
FGFSGVLATLPFAVWLFLAIEQLPLAAEESVDPKRDMPKGIILGMVTLMVSAFMIVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /trānslation="MDSSSGVSYKKADASYPEKRGLSRYAGVWSLWALGVGAVISGH
FSGWNFGFSTGGWGGMLVAGIIIAIMYLGLTFSIAEMSPALPHTGAAYSFARTAMGPW
                                                                                                                                                                                                                                                                                                                                                 NPSLPGVGAFHLSSSLEPLLDGFKAIYGDGGVVLLGLVALTGLIASFHTILYAQGRQI
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        note="identified by sequence similarity; putative; ORF
ocated using Blastx/Glimmer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ^note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer"
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Conservative:
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                                                                                                                                                               /protein_id="AAL43133.1"
/db xref="G1:17740607"
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/transl_table=11
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942.50
63.11%
43.33%
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                                                                                                                                                                                  note="identified by sequence similarity; putative; ORF located using Blastx/Glimmer"
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transI_table=11
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                                                                        Hinkle,G., Slater,S.C. and Goodner,B. Complete Genome Sequence of Agrobacterium tumefaciens C58 (Rhizobium radiobacter C58), the Causative Agent of Crown Gall Disease in Plants
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                                                                                                                                                                                                                                        Sidney Street
                                                                                                                                                                                                                                Submitted (14-AUG-2001) Cereon Genomics, 45 Cambridge, MA 02139, USA Location/Qualifiers
C58 (Cereon)
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transl table=
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AE008130 AE007869
AE008130.1 GI:15157274
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                                                                                                                                                              MetargSerValArgAsnLysteuGluGluAlaGlyIleLeuMetGluAlaThrHisPro
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                                                                                                                                                                                                                                                               244 AlaThrPheMetAlaLysLeuSerSerThrAlaLeuGlyAsnAlaCysHisIleHisMet
                                                                                                                                                                                                                                                                                                                                                                                                                            TyrPhePheAlaSerTyrIleAsnSerTyrLygArgLeuGlnProLeuThrPheAlaPro
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                                                                                164 ThralaGlnProHisHisGlnTrpMetAsnileSerAlaSerSerGlyIleGluThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerieuGlnAspAlaGluThrGluLysAsnAlaPheTyrAspGlnAsnAspGluTyrGly
                                                                                                                                                                                                                                          GluPheLeuProSerGlnHisGluLeuAsnPheValProAlaAspProLeuThrMetAla
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VFYAI FLALMVFGLELSFKVTLVITLISLAVLVFFWISAIPNIDFSRFALNIGVGPDG
KAVELPEGGGSFFPFGFSGVLATIPFAVWLFLAIEQLPLAAEESVDPKRDMPKGIILG
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LGAEQGGSIIGSVLLIMMAVEGAMESYIMQAISFILLRKNLPNIERPRSPFGSFGALL
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LLNVMIEIRNDLIANEGEQAAIAGFLHELMGKALSSIEE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSAAGTDVYFSHAPAEDRRGKSLRSTTATVSDVIHAHYDALTRSEKRLAESLLGNYPV
SGLGSITTIAENAGVSTPTVARMVQKLGYKGYPEFQAHLHQELBATISGPVAKHDRWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EYFFTHMQVIRPKTTLMSSNSSAWPQYMLNMSAGDVLVIFDIRRYBHDMTTLAEVAKA
NGVQIILFTDQWTSPVARHALHTFRVRIBAPSAWDSSVVTLFVVBALIBAVQNGTWDB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6080 crigicarcardeagagagacrerardagacaaacagireaagagaaaricricargaa 6021
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5960 ACCGTTCCCGGTTACAAGTCCTCGAGCTGGGGAAAAGGGATATGGCGATTATACGCTGAAG 5901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 ThrTyrAspGluLeuAsnAsnLeuIleArgAsnGlyLysileAspThrValValLeuAla 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 LeuAspGlnLysLysIleSerIleSerThrPheValTyrAlaValThrIleGluGlyIle 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 AlaGlyGlyGlyTyrGluIleSerSerValAspThrGlyTyrSerAspCysHisLeuCys 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||:::||| |||||||:::
| ACATTCGACGCACTTAAAATGGATGTCGCCGAGGGGGCGCATCGACACTGTTCTGGCCTGC
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complement (7956. .8729)
/gene="AGR C 3887"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8704. 9780
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8704. 9780
/gene="AGR C_3888"
/note="hypothetical protein PA5506 {imported}
Pseudomonas aeruginosa (strain PA01)"
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Indels:
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/note="hypothetical protein"
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                      /transī_table=11
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product="AGR C
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Best Local Similarity:
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LPQLVHKDPIDRILITTAREHDLTIITRDRVILAYGEAGHVKTLAC"
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complement (4788. .6152)
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FPADDGESAYVAPQILVNVDHSMEFWTEETFGPAIGIMKVKONDDEAIALMNDSKYGLT
ASLWTQDAARAARIGREIETGTVFMNRADYLDPALCWTGVKETGRGGSLSVLGFQNLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="MAMTGDQIDKSWFSQQLKRKGKSQADLARFLNLDRSAVTRMLNG
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STTESRHPIFGCMKGTITVMPDVDLTKPVDFEWGEKLYNE"
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AGYRLCGAETKGIRIECRVGGSDLNPYLAMAALLAAGIDGIENKLELEPAFVGDAYGG
KDVREIPKTLRDATAFLDGSKMLRQAFGDDVVDHYVHAARWEQEEYDRRVTDWEVARG
                                                                                                                                                                                                                  LLVGERMVRAFVEAGVPEDVFINVFLDHGTTSTLISEGLFNFVNFTGSVEGGRAIERA
                                                                                                                                                                                                                                           AAGTFTGLGLELGGKDPGYVMEDADLDAAVDTLMDGGTYNSGQCCCGIERIYVNENLY
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SLWALGVGAVISGHFSGWNFGFSTGGWGGMLVAGIIIAIMYLGLTFSIAEMSPALPHT
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complement [3888. .4334)
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/note="hypothetical protein"
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complement 76218. .7774)
/gene="AGR C 3885"
/note="probable transport pa
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protein id="AAK87888.1"
db_xref="GI:15157280"
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/gene="AGR C 3882"
complement (4297. .4725)
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transl_table=11
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/strain="H37Rv"
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Mycobacterium tuberculosis H37Rv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 13246)
Parkhill, J.
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            AlaAspLeuAsnSerLeuHisLeuLeuProTrpSerGluGlyAlaValLeuAla1leSer 103
                                                                                                                                     124 GlnGlnIleGluArgLeuAlaAsnLeuLysLeuLysGlyLeuPheAlaSerGluLeuGlu
                                                                                                                                                                5780 AAGCAGGTGGCGCGCGCGCGATGGGGCTGAAGGCCTATATGGCGACCGAACTAGAA
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Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
13246 bp DNA linear BCT 02-SEP-2002
Mycobacterium tuberculosis H37Rv complete genome; segment 125/162.
AL008883 AL123456
AL008883.1 GI:3261490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA Unite de Genetique Moleculaire Bacterienne, Institut Pereur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk On Jun 27, 1998 this sequence version replaced gi:2612801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E., Fetaia, F., Badcock, K., Badaham, D., Entillingworth, T., Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J., Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A., Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence
Nature 393 (6685), 537-544 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="fragment designated v003. Does not represent a physical clone"
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gene

CDS

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Probable glutamine synthetase class II, glnA4; similar to probable glutamine synthases eq. sp[P10656[GANA_CLOBB_many glutamine synthases eq. sp[P10656[GANA_CLOBB_many glutamine synthases eq. sp[P10656[GANA_CLOBB_many glutamine synthases [EC 6.3.1.2) [443 aa] Fasta scores; opt: 609 z-score: 750.0 E(): 0; 30.7% identity in 446 aa overlap; and GLNA_BACCE_P19064 glutamine synthetase (ec 6.3.1.2) [443 aa], fasta scores; opt: 572 z-score: 669.3 E(): 4e-30, 30.8% identity in 455 aa overlap. Also similar to M. tuberculosis glutamine synthases eg. MTCV427.03c [31.1% identity in 453 aa overlap.]
DGGDPLRPASPRLRSPLGASRPVVGLTAYLBQVRTGVWDIPAGYLPADYFEGITWAGG
YALLDPQPUDESVGCVLDSLAALVITGGYDLDPAAYQGBPHPATDBRPRGRDAWEF
ALLRGALQRGMPVLGICRGTQVLAVALGGTLHQHLPDILGHSGHRAGNGVFTRLPVHT
ASGTRLAELIGESADVPCYHHQAIDQVGEGLVVSAVDVDGVIEALELPGDTFVLAVQW
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GFRYDEALVTCDNHAIYKNGAKEIADQHGKSLIFMAKYDEREGNSCHIHVSLRGTDGS
AVPADSNGPHGMSSMFRSFVAGQLATLREFTLCYAPTINSYKRFADSSFAPTALAMGL
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YQGADVERLPVTLADAAVLFEDSALVREAFGEDVVAHYLNNARVELAAFNAAVTDWER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (3171519. .3171569) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (3171573. .3171613)"
                                                                                                                                                                                                                                                                                                                                                                                                    complement (3171465. .3171515) "
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/note="possible RBS upstream of Rv2860c"
                                                                                                                                                                                                                                                                            /note="possible RBS upstream of Rv2858c"
complement(2245. .2995)
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                                                                                                                                                            HPEKSLDDLRLFKALVDAASGYAGRQSQAEPR"
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Matches:
Conservative:
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Indels:
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|db_xref="G1:2612805"
|db_xref="SPTREMBL:033342"
                                                                                                                                                                                                                                                                                                                                                                                                    /note="FT repeat unit cocomplement(2999. 3049)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="FT repeat_unit complement(3053._.3093)
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complement(3104. .4477)
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                                                                                                                                                                                                          complement (2206. .2209)
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/transl_table=11
/product="glnA4"
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/note="FŢ repea
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799.50
58.02%
38.68%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Rv2858c, (MTV003.04c), len: 455 aa. aldC, Probablealdehyde dehydrogenase, aldC; similar to many eg. Probablealdehyde dehydrogenase, aldC; similar to many eg. FRAB ECOLI P80668 phenylacetaldehyde dehydrogenase (499 aa), fasta scores; opt: 1074 z. score: 1239. Z E(): 0, 42.2% identity in462 aa overlap. Contains P800687 Aldehyde dehydrogenases glutamic acid active site and P800070 Aldehyde dehydrogenases cysteine active site. Also similar to many M. tuberculosis dehydrogenases eg. MTCY369.13 (38.1% identity in 467 aa overlap)" (codon start=1 / codon start=1 / city in 25 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon start=1 / codon s
                                                                                                                                                                                                                                                                                                                                                                                                                                     EAGGAAADELSGLFVPTDVCDEDAVNGLFDGAAETYGRIDIAFNNAGISPFEDNLIEN
TELAAWGVODVNLKSYYLCCRAALHHVLAGKGSINYTASFYNAWGSATSQISYTAS
KGGVLAMSRELGVOPARQGIRVNALCPGPVNTPLLQELFAKNPERAARRMYHVPLGRF
AEPDEIAAAVAFLABDDASFITASTFLVDGGISSAYVTPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTTMRLGELAVEAGLDEDLLQVLPGKGTVVGERFVTHPDIRKIVFTGSTEVGKRVMAG
AAAQVKRVTLELGGKSANIVPHDCDLERAATTAPAGVFDNAGQDCCARSRILVQRSVY
DRFMELLEPAVHSIVVGDPGSRATEMGPLVSRAHRDKVAGYVPDDAPVAFRGTAPAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="SPTREMBL:033341"
/translation="MDLSASRSDGGDPLRPASPRLRSPVSDGGDPLRPASPRLRSPVS
                                                                                                                                                                                                                                                                                                                                                              /db_xref="SPTREMBL:033339"
/translation="MMDLSQRLAGRVAVITGGGSGIGLAAGRRMRAEGATIVVGDVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFWFPPTVLTPKRGDRTVTDE1FGPVVVVLTFDDEADA1SLANDTAYGLSGS1WTDDL
SRALRVARAVESGNLSVNSHSSVRFNTPFGGFKQSGVGRELGPDAPLQFTETKNVFIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tränslation="MSTTQLINPATEEVLASVDHTDANAVDDAVQRARAAQQRRWARLA
PAQRAAGLRAFAAAVQAHLDELAALEVANSGHPIVSAEWEAGHVRDVLAFYAASPERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGRQIPVAGGVDVTFNEPMGVVGVITPWNFPWVIASWAIAPALAAGNAVLVKPAELTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similar to E. coli hypothetical gene TR:P76038 (EMBL:AE000228) (258 aa), fasta scores; opt: 326 z-score: 354.5 E(): 1.4e-12,30.7% identity in 238 aa overlap. Contains three 17 aa repeats at the N-terminus very
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similar to those in other M. tuberculosis proteins e.g. YY30_MYCTU Q10699 putative DNA polymerase CY49.30 (393:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="PS00070 Aldehyde dehydrogenases cysteine active
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                                         overlap. Also similar to many M. tuberculosis
dehydrogenases eg. MTCY39.16c (38.3%identity in 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="Rv2859c, (MTV003.05c), len: 308 aa. Unknown;
    632.1 E(): 4.7e-28, 38.0% identity in 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="possible RBS upstream of Rv2857c"
complement(1400, .1435)
/gene="aldC"
                                                                                                                                                                                                                  /product="hypothetical protein Rv2857c"
(protein_id="CAA15519.1"
db_xref="GI:2612802"
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'transT_table=11
'product="hypothetical protein Rv2859c"
protein_id="CAA15521.1"
db_xref="G1:2612804"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAA15520.1"
/db_xref="GI:2612803"
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/gene="Rv2859c"
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trans1 table=11
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13246 176 88 180 11

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EAGGAAADELSGLFVPTDVCDEDAVNGLFDGAAETYGRIDIAFNNAGISPPEDNLIEN
TELAAWQRVQDVNLKSVYLCCRAALRHMVLAGKGSIVNTASFVAVMGSATSQISYTAS
KGGVLAMSRELGVQPARQGIRVNALCPGPVNTPLLQELFAKNPERAARRMVHVPLGRF
                                                                                                           27-APR-2001
of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 14715)
Felsischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains
                LeuGluLeuproProProAlaSerGlyAsnValTyrAsnAspLysGluLeuProGluPhe 398
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis CDC1551
Mycobacterium tuberculosis CDC1551
Bacteria; Actinobacteria Actinobacteridae; Actinomycetales;
Corymebacterineae; Mycobacteriaceae; Mycobacterium, Mycobacterium
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Submitted (25-APR-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
Location/Qualifiers
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Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Piller, M., Mikula, A. and Bishai, W.
                                                                                                                                                                           3214 TTCGGCGAGGATGTTGTCGCGCACTACCTGAACACGCGCGTGTGGAGCTGGCGGCGTTC
                                    3334 CTTCAGCTGCCCGAGCCCTGTGGCAACGCCTACCAAGGCGCCGATGTCGAACGGCTG
                                                                                     ProAsnSerLeuGlnAsnAlaThrHisLeuLeuLysGluSerLysMetLeuAsnLysThr
                                                                                                                                                         PheGlyGluLysLeulleLeuHisTyrValAsnAlaAlaAsnValGluIleAsnGluPhe
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AE007117 AE00516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to GB:AE000512; identified similarity; putative" codon start=1 /trans1_table=11
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complement (921. .2288)
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/product="oxidoreductase, short-dehydrogenase/reductase family"
/protein_id="AAK47250.1"
/db_xref="GI:13882700"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .14715
/organism="Mycobacterium
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/strain="CDC1551"
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/note="clinical strain"
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Unpublished
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KEYWORDS
SOURCE
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AE007117/c
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AUTHORS
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JOURNAL
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                                                                                                                           3865 GAGGCGGTCAAAGGCGAATGCAACATGGGCCAGCAGGAGATCGGGTTTCGTTACGACGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3451 GTGGTT---GGCCACGGCCAAAACATCCGGTCGAATGCCGGGTTCCCGGCGGTGATGTC 3395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1453 TTGGCGTGGACCGAGTTGGAGCGACTGGTCGCGGCCGGTGACGTCGACACCGTCATCGTC 4394
                                                                                                                                                                                                  1213 ATGACGCCGGÁCTTGTCCACTCTGCGCCTGATTCCTTGGCTACCGGGÁACGGCGCTGGTG 4154
                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 AlaSerGluLeuGluPheAsnLeuPheAsnGluThrTyrLysSerAlaSerGlnLysHis 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 ValProGluAlaThrTyrPhePheAlaSerTyrIleAsnSerTyrLysArgLeuGlnPro 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AsnProTyrLeuAlaPheSerAlaIleIleAlaAlaGlyIleSerGlyIleGluGluLys 378
                                                                                                                                                                                                                                                LeuCysAlaAspLeuAsnSerLeuHisLeuLeuProTrpSerGluGlyAlaValLeuAla 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlylleGluThrPheMetArgSerValArgAsnLysLeuGluGluAlaGlylleLeuMet 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CysHisIleHisMetSerLeuGlnAspAlaGluThrGluLysAsnAlaPheTyrAspGln 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuCysAsnSerLysSerGluGlyIleAsnValGluLeuArgIleGlyGlyAlaAspLeu 358
                                   42
                                                                                                       61
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                                                     ---GlyLeuAspGlnLysLysIleSerIleSerThrPheValTyrAlaValThrIleGlu
                                                                                                                                                                          GlylleAlaGlyGlyTyrGlulleSerSerValAspThrGlyTyrSerAspCysHis
                                                                                                                                                                                                                                                                                                                      102 IleSerAsnProHisAsnPheValThrSerGluProLeuPheCysSerProArgValIle
                                                                                                                                                                                                                                                                                                                                                                                           LeuMetGlnGlnIleGluArgLeuAlaAsnLeuLysLeuLysGlyLeu-----Phe
                                                                                                                                                                                                                                                                                                                                                                                                               |||| :::|||:::::|||| CTGCGCCGCGCGCGACTGGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TrpLysAsnLeuLysThrAlaGlnProHisHisGlnTrpMetAsnIleSerAlaSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3985 TATCGCGGGCTGACCCCGGCCAGCGACTACAACATCGACTACGCGATATTGGCATCTTCG
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TTGGGGAATTCACGCTGTGTATGCGCGACCATTAACTCCTACAAGCGATTTGCCGAT
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LGSIELDLVKARRAGEVVVIELDMWFGSLEWRLPNGASASIDDVEVYVGSASDRRKDA
PAEGTPHVVLTGRWVGSVVIKGPRAALLRRHRG"
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ACCORRGVTRIKTFDHTLASAFRS"
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BOTGTVAXTRSBWHLPKDRIWYDGQLKMARDBGRWHYRWTTSGLHPKKGBHQTFALRA
DPPRRASVNEVGGTDVLVPGYLYHYSLDAGQAGRELFGTAHAVGALHPFDDTLNDPQ
LLABQASSSTQPLDLVTLHADDSNRVAAAIGQLPGVVITPQABELPTDKHFAPNVLND
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TRGGKAMIVVIKPSTGEILAIAQNAGADADGPVATTGLYPPGSTFKMITAGAAVERDL
ATPETLLGCPGEIDIGHRTIPNYGGFDLGVVPMSRAPASSCNTTFAELSSRLPPRGLT
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HCREDSRWQLVEVSTRGCGEPHGVRHRSVGASRDAEFGADLVFAVGAAGGNVGVGFSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MSRPVSPSQFLTSATMVTKTTLASATSGLLLLLAVVAMSGCTPRP
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GEAEFPGGSHSWFAGYRGDLAFASLIVGGGSSEYAVRMTKVMFESLPPGYLA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="penicillin-binding protein, putative"
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/note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ^motes"identified by Glimmer2, putative"
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                                                                                            note="identified by Glimmer2; putative"
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                                                                                                                                                                                                                     /protein_id="AAK47255...
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/transl_table=11
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/gene="MT2931"
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/gene="MT2932"
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/gene="MT2932"
/gene="MT2930"
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                                CDS
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GYLPADYFEGITWAGGVAVILPPQPVDPESVGCVLDSLHALVITGGYDLDPAAYGGEP
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GHRAONGVFTRLPPUTASGTRLAELIGESADVPCYHHQAIDQVGEGLVVSAVDVDGVI
EALELPGDTFVLAVQMHPEKSLDDLRLFKALVDAASGYAGRQSQAEPR"

COMPLEMENT (3138 - 4511)
                                                                                                                                                                                                                  product="aldehyde dehydrogenase family protein"
protein.id="AAK47251.1"
db xref="G1:13882701"
translation="MSTTQLINPATEEVLASVDHADANAVDDAVQRARAAQRRWARLA
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAQVKRVTLELGGKSANIVFHDCDLERAATTAPAGVFDNAGQDCCARSRILVQRSVY
PORPAYHSIVYGDPGSRATREMGPLYSRAHBOKVASVYDDDAPVARGTAPAGR
GFWFPFTVLFPKRGDRTVTDEIFGPVVVVLFDDEADAISLANDTAYGLSGSIWTDDL
SRALRVARAVESGNLSVNSHSSVRFNTPFGGFKQSGVGRELGPDAPLQFTKNVFIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="WTGPGSPPLAWTELERLVAAGDVDTVIVAPTDMOGRLAGKRISG
RHFVDDIATRGVECCSYLLAVDVDLMTVPGYAMASWDTGYGDMVMTPDLSTLRLIPWL
PGTALVIADLVWADGSEVAVSPRSILRRQLDRLKARGLVADVATELEFIVFDQPYRQA
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GRRYDEALVYCDNHAIYKNGAKEIADQHGKSLTPWAKYDEREGNSCHTHVSLAGTDGS
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DNRTCALRVYGHGGNITVECRPYGGVNYATAAILAGGLYGIERGLQLPEPCVGNA
YQGADVERLPVTLADAAVLFEDSALVREAFGEDVVAHYLNNARVELAAFNAAVTDWER
                                                                                                                                                                                                                                                                                                                                                                                                              LTTMRLGELAVEAGLDEDLLQVLPGKGTVVGERFVTHPDIRKIVFTGSTEVGKRVMAG
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PID:473823; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /trānslation="MPSRTALSPGVLSPTRPVPNWIARPEYVGKPAAQEGSEPWVQTP
EVIEKMRVAGRIAAGALAEAGKAVAPGVTTDELDRIAHEYLVDNGAYPSTLGYKGFPK
                                                                                                                                                                                                                                                                                                                                               PAQRAAGLRAFAAAVQAHLDELAALEVANSGHPIVSAEWEAGHVRDVLAFYAASPERI
SGRQIPVAGGVDVTFNEPMGVVGVITPWNFPMVIASWAIAPALAAGNAVLVKPAELTF
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DRTREATMRAINTVKPGRALSVIGRVIESYANRFGYNVVRDFTGHGIGTTFHNGLVVL
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GB:AE000512; identified by sequence similarity; putative"
                                                                                        note="similar to PID:2228233; identified by seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to GP:3581870; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="glutamine amidotransferase, putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       producE="glutamine synthetase, putative"
protein_id="AAK47253.1"
db_xref="GI:13882703"
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product="methionine aminopeptidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein_id="AAK47252.1"
db_xref="GI:13882702"
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db_xref="GI:13882704"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (2285. .3085)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (2285. .3085)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (4671. .5528)
                          complement (921. .2288)
/gene="MT2926"
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1605 TIGCGCGAATICACGCIGIGCTAIGCGCCGACCATIAACTCCTACAAGCGATITGCCGAT 3546
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Mycobacterium bovis subsp. bovis AF2122/97
Mycobacterium bovis subsp. bovis AF2122/97
Mycobacteria, Actinobacteria, Actinobacteriaes, Actinomycetales,
Corynabacterinaes, Mycobacteriaceae, Mycobacterium
tuberculosis complex.
                                                              3545 AGCAGTÍTCGCGCCGACGCCTGGCTTGGGGGCTGGACAATCGCACCTGCGCCTGCGG
                                                                                                339 LeuCysAsnSerLysSerGluGlyIleAsnValGluLeuArgIleGlyGlyAlaAspLeu
                                   319 LeuThrPheAlaProThrLysCysCysTrpAlalleAspAsnArgThrSerAlaPheArg
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/Longlement(9): 18,75/
/Lougle tag="Mb2882c, -, len: 258 aa. Equivalent to Rv2857c, |
/Loce="Mb2882c, -, len: 258 aa. Equivalent to Rv2857c, len: 258 aa, from Wycobacterium tuberculosis strain H37Rv, len: 258 aa, from Wycobacterium tuberculosis strain H37Rv, len: 258 aa, from Wycobacterium tuberculosis strain H37Rv, len: 258 aa, from Straptomyces coelical dehydrogenases reg. (Bolley 1, 1941). Thighly similar to various dehydrogenases e.g. 088068 |SC135,33c PROBABLE DEHYDROGENASE (SDR FAMILY) from Straptomyces coelicalor (260 aa), FASTA scores: opt: 1089, El; 2.1e-28, (12.31$ identity in 253 aa overlap); Q91376 |PA1649 from Pseudomonas aeruginosa PROBABLE SHORT-CHAIN DEHYDROGENASE (253 aa), FASTA scores: opt: 569, El; 2.1e-28, (13.2$ identity in 255 aa overlap); Q9EX74 |MLHA SDR-LIKE ENZYME from Rhodococcus erythropolis (246 aa), FASTA scores: opt: 567, El; 2.5e-28, (13.2$ identity in 258 aa overlap); etc. Also similar to many Mycobacterium tuberchlosis dehydrogenases e.g. FABG3 |Rv2002 |MT2058 |MTCY39.16c PUTATIVE OXIDOREDUCTASE (260 R), FASTA score: (18.3$ identity in 248 aa overlap). BELONGS TO THE SHORT-CHAIN (ENTAND SERONGS CORD) BELONGS TO THE SHORT-CHAIN (ENTAND SERONGS CORD) ENTAND CENTAND CENTAND CORD FAMILY."
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db_xref="G1:31619629"
'translation="MMDLSQRLAGRVAVITGGGSGIGLAAGRRMRAEGATIVVGDVDV
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TELAAWQVQDVNLKSYYLCCRAALHNVLAGKSIVYTASFYAVWGSATSQISYTAS
KGGVLAMSRELGVOFARQGIRVNALCPGPVATPLLQELAKNPERAARRMVHVPLGRF
AEPDEIAAAVAFLASDDASFITASTFLVDGGISSAYVTPL"
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PAQRAAGLRAFAAAVQAHLDELAALEVANSGHPIVSAEWEAGHVRDVLAFYAASPERL
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EC number="1.2.1.3"
note="Mb2883c, aldC, len: 455 aa. Equivalent to Rv2858c,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             trans]_table=11
product="PROBABLE ALDEHYDE DEHYDROGENASE ALDC"
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/transl_table=11
/product="PROBABLE SHORT-CHAIN TYPE
DEHYDROGERASE/REUUCTASE"
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db_xref="G1:31619630"
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complement(872. .2239)
/gene="aldC"
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gene

CDS

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/EC_number="6.3.5."
/EC_number="6.3.5."
/EC_number="6.3.5."
/EC_number="6.3.5."
// NoTe="Mb2884c, -, len: 308 aa. Equivalent to Rv2859c, len: 308 aa. from Wycobacterium tuberculosis strain H37Rv, (100.0% identity in 308 aa overlap). Possible amidotransferase (EC 6.3.5. or 2...-), equivalent (but longer 58 aa) to 09CEU9/ML1573 POSSIBLE ANIDOTRANSFERASE from Mycobacterium leprae (249 aa), FASTA scores: opt: 1226, E(): 3e-64, (71.55% identity in 239 aa overlap). Also similar to other amidotransferases and hypothetical proteins, but shorter in N-terminus e.g. O88072[SCI35.37] HYPOTHETICAL 25.3 KDA PROTEIN from Streptomyces coelicolor (242 aa), FASTA scores: opt: 683, E(): 1.2e-32 (47.65% identity in 235 aa overlap); AAK7320|Q97488|CAC1764 PREDICTED GLUTAMINE AMIDOTRANSFERASE from Clostridium acetobutylicum (241 aa), FASTA scores opt: 458, E(): 1.6e-19, (32.95% identity in 246 aa overlap); AAK7520|Q9709|SP1089 GLUTAMINE AMIDOTRANSFERASE CLASS I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /EC number="6.3.1.2"
//note="Mb2885c, glnA4, len: 457 aa. Equivalent to Rv2860c, len: 457 aa, from Mycobacterium tuberculosis etrain H37Rv, len: 457 aa, from Mycobacterium tuberculosis etrain H37Rv, (100.0% identity in 457 aa overlap). Probable glnA4, glutamine synthetase class II (EC 6.3.1.2), similar to many glutamine synthases e.g. O88070[SCI35.35c from Streptomyces coelicolor (462 aa), FASTA scores: opt: 1947, E(): 8.2e-120, (64.15% identity in 452 aa overlap); 098H15[ML13074 from Rhizobium loti (Mesorhizobium loti) (456 aa), FASTA scores: opt: 1321, E(): 7.8e-79, (46.7% identity in 452 aa overlap); 098EM0[MLL187 from Rhizobium loti) (456 aa), FASTA scores: opt: 698, E(): 4.6e-38, (33.5% identity in 454 aa overlap); 09CD19[GLNA from Lactococcous lactis (446 aa), FASTA scores: opt: 633, E(): 8.2e-34, (32.45% identity in 456 aa overlap); etc. Also similar to three other potential glutamine synthases
LTTMRLGELAVEAGLDEDLLQVLPGKGTVVGERFYTHPDIRKIVFTGSTEVGKRVMAG
AAAQVKRVTLELGGKSANIVFHDCDLERAATTAPAGVFDNAGQDCCARSRILVQRSVY
DRFMELLEPAVHSIVVGDPGSRATEMGPLVSRAHRDKVAGYVPDDAPVAFRGTAPAGR
                                                                                                                               GFWFPPTVLTPKRGDRTVTDEI FGPVVVVLTFDDEADAI SLANDTAYGLSGSIWTDDL
SRALRVARAVESGNLSVNSHSSVRFNTPFGGFKQSGVGRELGPDAPLQFTETKNVFIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from Streptococcus pneumoniae (229 aa), FASTA scores: opt: 431, E(): 5.6e-18, (34.75% identity in 236 aa overlap); etc. Contains three 17 aa repeats at the N-terminus very similar to those in other Mycobacterium tuberculosis proteins e.g. 010699 | YY30 MYCTU | Rv2090 | MT2151 | MYCT49.30 PUTATIVE 5'-3' EXONUCLEASE RV2090 (EC 3.1.11.-)."
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DGGDPLRPASPRLRSPLGASRPVVGLTAYLEQVRTGVWDIPAGYLPADYFEGITWAGG
VAVLLPPQPVDPESVGCVLDSLHALVITGGYDLDPAAYGQEPHPATDHPRPGRDAWEF
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ASGTRLAELIGESADVPCYHHOAIDQVGEGLVVSAVDVDGVIEALELPGDFFVLAVQW
HPEKSLDDLRLFKALVDAASGYAGRQSQAEPR"
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101038|GANZ MYCTU|GLMA2|RV222c|MT2280|MTCY190.33c|MTCY427

03c PROBABLE GLUTAMINE SYNTHETASE (446 aa), FASTA score:

(31.1% identity in 453 aa overlap); Rv1878|glnA3 and
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protein id="CAD96571.1"
db_xref="G1:31619631"
                                                                                                                                                                                                                                                                                                                                  locus tag="Mb2884c"
EC_number="?
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complement(3143. .4516)
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complement(2236, .31
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Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)
                                                                                                                                                                                                                                                                                                                                                                                              339 LeuCysAsnSerLysSerGluGlyIleAsnValGluLeuArgIleGlyGlyAlaAspLeu 358
                                                                                                                                                                                                                          ValProGluAlaThrTyrPhePheAlaSerTyrIleAsnSerTyrLysArgLeuGlnPro 318
                                                                                                                                         AsnAspGluTyrGlyMetSerThrLeuAlaArgAsnTrpIleAlaGlyLeuLeuLysTyr 298
        cagcacggcaagagccraacgricarggcgaaracgargaaggggaa---ggraaragc
                                                                               3490 GTGGTT---GGCCACGGGCAAAACATCCGGGTCGAATGCCGGGTTCCCGGCGCGTGATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359 AsnProTyrieuAlaPheSerAlaIleIleAlaAlaGlyIleSerGlyIleGluGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277000 bp DNA linear BCT 11-FEB Streptomyces coelicolor A3(2) complete genome; segment 6/29. AL939109 AL031541 AL096811 AL096849 AL132648 AL137778 AL157953 AL499607 AL590507 AL645882
                                                                                                                                                                 319 LeuThrPheAlaProThrLysCysTrpAlalleAspAsnArgThrSerAlaPheArg
                                                                                                                                                                                                                                                                                                                                       3433 AACCAGTACCTGGCGGCGCGCTCTCATTGCTGGAGGGTTGTACGGTATCGAGCGGGC
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                                                     CysHisIleHisMetSerLeuGlnAspAlaGluThrGluLysAsnAlaPheTyrAspGln
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Streptomyces coelicolor A3(2)
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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Bentley, S.D.
Direct Submission
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                                                                                                                                           /translation="MTGPGSPPLAWTELERLVAAGDVDTVIVAFTDMQGRLAGKRISG
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WASGYRGLTPABJYNIDYAILASSRMEPLLRDIRLGWAGAGILRPBAVKGECNMGQQEI
GFRYDBALVTCDNHAIYKNGAKEIADQHGKSLIFPMAKYDEREGNSCHIHVSLRGTDGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlnSerGlyMetValAlaThrPheMetAlaLysLeuSerSerThrAlaLeuGlyAsnAla 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42
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GLUTAMINE SYNTHETASE FAMILY
                                                           (GLUTAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaCysValAspMetGlnGlyArgLeuMetGlyLysArgLeuThrGlyArgHisPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGTTCACCGACATGCAGGGCCGGCTGGCCGGCAAACGGATATCGGGCCGGCATTTCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGAACACGGTGCCCGGCTATGCGATTGGGACACGGCTACGCGATATGGTG
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                                                           SYNTHETASE GLNA4
                                                                                                                                                                                                                                                                                                                                       Matches:
Conservative:
Mismatches:
Indels:
                   /codon_start=1
/transl_table=11
/product="PROBABLE GLUTAMINE
SYNTHASE] (GS-II)"
TO THE
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                                                                                                 /protein_id="CAD96572.1"
/db_xref="GI:31619632"
  BELONGS
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799.50
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38.68%
33.65%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MTTILVTGGTGTLGRLVTERLRTGGHEVRVLSRHSEPYAVDLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGSGLDAALAGVDTVVHCATTQRGGDERSAANLIAAARRAGATHIVYISIVGVDRVPL
SYRBKXARDEKLVAESGIGMTVLRATQPHDLVVQMLRALAKLPVVVLPAHASDQPVEV
AEVADRLAELAAQGAPGRVPDMGGPEVRTFASLARAYLGATGRRRAVNVPLAGRTYR
AFRAGGHLAPEHAVGEGTFEEVLAGRFGHREGGRRRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MDPAARAVLEVALCVAPAALHEHLLRDFGGAGIALAVMLCAAV
ATMERRLVLTSPVACPDSSVARLLFHARHLEPLSAGGAAGFMAPLGTAVLLPTVLGWP
AADGTAFAEPGSAGTGRRPG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="SCL6.02, hypothetical protein, len: aa, similar to various hypothetical proteins, e.g. TR:CAB5258
[EMBL:AL10950] Streptomyces coelicolor hypothetical 25.2 kD protein, SCJ4.24c, 242 aa, fasta scores: opt: 48 a coverlap and to TR:O9EWP2 (EMBL:AL451182) Streptomyces coelicolor hypothetical protein SCK13.32c, 263 aa, fasta scores: opt: 11 Z-score: 779.3 E(): 8.9e-36; 49.407%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="putative ROK-family transcriptional regulatory
Submitted (09-MAY-2002) Submitted on behalf of the Streptomyces sequencing team, Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A E-mail: subdesnager. ac.uk
On or before Oct 29, 2002 this sequence version replaced
gi:20520886, gi:20520900, gi:20520927, gi:20520938, gi:20520939,
gi:20520886, gi:20520914, gi:20520916.
Location/Qualifiers
1. 277000
//organism="Streptomyces coelicolor A3(2)"
/mol type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/transl_table=11
/transl_conserved hypothetical protein SCL6.02"
/product=-conserved hypothetical protein SCL6.02"
/protein.id="CAB76867.1"
/db_xref="GI:7209205"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="possible integral membrane protein"
protein id="CAB76868.1"
db xref="GI:7209206"
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complement(1454. .2653)
/gene="SCO1447"
                                                                                                                                                                                                                                                                                                                                                                                                                      note="synonym: SCL6.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="synonym: SCL6.03"
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                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:100226"
226. .993
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/gene="SCO1447"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon start=1
transl table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="SC01445"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1064. .1432
/gene="SC01446"
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transī table=1
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/note="SCIG.06c, hypothetical protein, len: 152 aa;
similar to SW YBGC ECOLI (EMB1:MIG489) Escherichia coli
similar to SW YBGC ECOLI (EMB1:MIG489) Escherichia coli
region YBGC, 134 aa; fasta scores: opt: 140 z-score: 193.8
E(): 0.0023; 26.7% identity in 116 aa overlap"
/translation="MPASPSTARAINDRLALHLLQREGPLTAGQLKQLTGLSRPTVAD
LVERLTASGLIEVAGESGEQRRGPNAKLYGIVAERAYLAALDVRTEGVAVLVSDLLGR
                                                                              STGLPEWHRRLMAALQEKFPEARVGVENETNLAALAEQRDGAARDRDTFVLLWLGGI
GAAVVLUGTLRRGVSGGAGETGFWPVOETAGLPSATDCDGGFRSVAGAAAVTALAAEH
GVTRAFPAGFEPHAALVREAVRRSASGSDPAAERFLDALADRVVLGAAAVVLDPGC
LVLAGEI GRAGADALADRVQHRLTRMSPLATEVRPSTLGGGAVLRGALLTARDRAQDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mwtGTYGRREVRHARYAVAAVFAVHGSVTGSFATRVPWIODHAG
VSAGQLGIALAFPALGASLAMPLAGRVTHRFGARAALRGLLALWTLALALPSLAPNLL
TLCLALFVYGATAGMSDVAMNALGVEIETRLDKSIMSGLHGWMSTGALIGSAAGTLAA
                                                 VLAEASVPIDDHSGTGPAVEQAVSLVERAVKEAGADRLHTVGIGAPGLIDPAGGELRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLGTDARTHHLIAAAVLTVTGLVACTWVLDLQPAEDEDPPPRFALPPKSALLIGAVGF
VAVFREGAELDWSAYYLADELETSAGLAACTTGFTLTWALARLAGDKVDRFGAVRT
VRVSGVLATLGGLLVVVGGHPAVAWTGFALWGLGIAVVPLCFAAAGRAGSPSLAIA
GVATITYSGLVAPSAIGGLAQATSLVVSFGLVTLLACCLVVFAKVLRAGDRNRFKIS
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WTELWAGHGVRFEGDWEAAGDACNAVRELTIGYEAPVTRPGAYAVHLWLDRLGTTGLT
YGPRFCSADGATTYARGTRVLVRLDARTLRPAPWSEAFRTAGRALLRPAD"
                                                                                                                                                                                                                                                 /gene="SCO1447"
/note="Pfam match to entry PF00480 ROK, ROK family, score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4564. .6000
/gene="SCO1450"
/note="SCL6.07, probable uracyl permease, len: 478 aa;
similar to TR:BAA35783 (EMBL:D90738) Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="PS00217 Sugar transport proteins signature 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/transl_table=11
/product="putative transport protein"
/protein_id="CAB76870.1"
/db_xref="GI:7209208"
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/protein id="CAB76871.1"
/db xref="GI:7209209"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="synonym: SCL6.06c"
complement (3937. .4395)
/gene="SCO1449"
                                                                                                                                                                                                                                                                                                                                                                                    2766. .3977
/gene="SCO1448"
/note="synonym: SCL6.05"
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                                                                                                                                                                                                                    complement (1934. .2104)
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/gene="SCO1449"
                                                                                                                                                                                                                                                                                                     45.80, E-value 1.5e-12"
complement (2662. .2667)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2766. .3977
/gene="SCO1448"
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/gene="SCO1448"
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/gene="SCO1450"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=]
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183290

183182

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182827 GAGGTCGCCCACTACCGGAACATGCCCCCCGTCGAACTGGACGCCTTCGACGCCGC 182768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BCT 10-MAY-2003
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      201
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                                         183466 AAGGGGAAGTGCAACCCGGCCAGCAGCACGACTCCGCTACGACGAGGCCCTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 HisMetSerLeuGlnAspAlaGluThrGluLysAsnAlaPheTyrAspGlnAsnAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182944 CCCGAGCCTGCCCCGGCAACGCGTACACC---GCCGACTTCGCGCACGTCCCCACCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 ThrPheMetArgSerValArgAsnLysLeuGluGluAlaGlyIleLeuMetGluAlaThr
                                                                                                                                                                                                                                                                                      183406 ACCTGCGACCAGCACGCGTCTACAAGACCGGGCGCAAGGAGATCGCCGCCCAGGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                        302 AlaThrTyrPhePheAlaSerTyrIJeAsnSerTyrLysArgLeuGlnProLeuThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183121 GCCCCACCGCCGTCGCCTGGGGCCACGACAACCGCACCTGCGCCCTGCGCGTCGTC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183064 GGCCACGGCCCCCCCCCCTTCGAGAACCGGCTCCCCGGCGGCGCGTCAACCCCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuGlnAsnAlaThrHisLeuLeuLysGluSerLysMetLeuAsnLysThrPheGlyGlu
                                                                                                                              HisProGluPheLeuProSerGlnHisGluLeuAsnPheValProAlaAspProLeuThr
                                                                                                                                                                                                                                                                                                                                                                        MetValAlaThrPheMetAlaLysLeuSerSerThrAlaLeuGlyAsnAlaCysHisIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282 TyrGlyMetSerThrLeuAlaArgAsnTrpIleAlaGlyLeuLeuLysTyrValProGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeualaPheSeralallelleAlaAlaGlyIleSerGlyIleGluGluLyBLeuGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProProProAlaSerGlyAsnValTyrAsnAspLysGluLeuProGluPheProAsnSer
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Streptomyces avermitilis genomic DNA, complete genome, section
27/30.
                                                                                                                                                                                                                                                   MethlaAspArgHisIlelleAlaLysHisGlyValArgGluMetAlaGluGlnSerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       342 SerLysSerGluGlyIleAsnValGluLeuArgIleGlyGlyAlaAspLeuAsnProTyr
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Shinose,M., Takahashi,Y., Horikawa,H., Nakazawa,H., Osonoe,T.
Kikuchi,H., Shiba,T., Sakaki,Y. and Hattori,M.
Genome sequence of an industrial microorganism Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces avermitilis MA-4680
Streptomyces avermitilis MA-4680
Bacteria; Actinobacteria; Actinobacteria Actinobacteria Streptomyces.
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TYWPQDQWTALFVMLFTGLAVVCLRGFWSRIAIFLGLVFGYVLSWALDRIFGKIHSVD
GSGKPTDHWRLDFSAVGQADWIGLPSFHGPSFEWSAILVALPVVIALIAENAGHVKAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEMTGDNLDDKLGTAISADGIGSVLSTAVGGPPNTTYSENIGVMAATRYYSTAAYWAA
AGFALLFGLCPKFGAVVAAIPGGVLGGITVILYGMIGLLGAQIWINAKVDMRNPLNLV
PAAAGIIIGVGNVSMEFTDTFSLSGIALGTLVVITGYHALRAFAPAHLKTQQPLLDEG
                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MDLGVRWKLHGDGKVPAPGAVVRPDERLSWPRTAGLGAQHVVAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FGASFVAPVLMGLDPNLAIMMSGVATVIFLLATRGRVPSYLGCSLSFVGVAAVIRAQG
uracil transport protein PyrP, 442 aa; fasta scores: opt: 908 z-score: 949.9 E(): 0; 43.1% identity in 429 aa overlap and to SW:PYRP_BACCL (EMBL:X76083) Bacillus caldolyticus uracil permease (uracil transporter) PyrP, 432 aa; fasta scores: opt: 770 z-score: 806.6 E(): 0; 31.0% identity in 437 aa overlap. Contains Pfam match to entry PF00860 xan ur permease, Xanthine, uracil permeases family. Contains also possible hydrophobic membrane spanning regions.
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/gene="SCO1450"
/note="Pfam match to entry PF00860 xan_ur_permease,
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/rsans_table=11
product="putative uracyl permease"
protein_id="CAB76872.1"
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/note="SAV6515"
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/transl_table=
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/gene="aroH"
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Sakaki, Y. and Hattori, M.
Direct Submission

L. Submitted (199-MAR-2002) Director-General of Biotechnology Center,
Direct Submission

L. Submitted (199-MAR-2002) Director-General of Biotechnology Center,
National Institute of Technology and Evaluation, Biotechnology
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This work was done in collaboration with Haruo Ikeda(*1), Jun
Ishikawa(*2), Akiharu Hanamoto(*3), Chiquea Takahashi(*3), Mayumi
Shinose(*4), Norihiro Kushida(*4), Hisashi Kikuchi(*4), Tomomi
Osonoe(*4), Norihiro Kushida(*4), Hisashi Kikuchi(*4), Tadayoshi
and Satoshi Omura(*1,*3).

Final finishing process and all annotation were done by H. Ikeda
and J. Ishikawa.
                                                                                                                                                                   Ikeda,H., Ishikawa,J., Hanamoto,A., Shinose,M., Kikuchi,H., Shiba,T., Sakaki,Y., Hattori,M. and Omura,S.
Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis
Nat. Biotechnol. 21 (5), 526-531 (2003)
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PDRDPRMRVVSVAYTALLPDPPEPHGGGDAAQAQWLRYNALGPLAFDHDR1LADAHER
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                                                                                                                                                                                                                                                                                                                                                   3 (bases 1 to 298550)
Omura,S., Ikeda,H., Ishikawa,J., Hanamoto,A., Takahashi,C.,
Shinose,M., Takahashi,Y., Horikawa,H., Nakazawa,H., Osonoe,T.,
Kushida,N., Director-General of Biotechnology Center, Shiba,T.
                                                             Proc. Natl. Acad. Sci. U.S.A. 98 (21), 12215-12220 (2001) 21477403
avermitilis: deducing the ability of producing secondary metabolites
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/note="This strain is also named as strain: ATC
NCIMB 12804 or NRRL 8165.~synonym: Streptomyces avermectinius"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *3 The Kitasato Institute
*4 National Institute of Technology and Evaluation
*5 School of Science, Kitasato University
*6 Institute of Medical Science, University of Tokyo
*7 RIKEN, Genomic Sciences Center
Pollowing url is also available.

http://avermitiis.ls.kitasato-u.ac.jp.
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/mol type="genomic DNA"
/strain="MA-4680"
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(protein_id="BAC74224.1"
(db_xref="GI:25510177")
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                                                                                                                                                                                                                                                                           RAVPVVMDADAHDRAVALVSHMPHLVSSMVAARLENAEETAVRLCGGGIRDVTRIAAS
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GNAGOVRVPGKHGSPRTYETVAVIIDDQPGGLARIFADAGLAGVNIEDVRIEHATGQ
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ARAARRSGELKGADVNSTREALLKRDAADSSRKTSPLAKADDAVEVDTSDLTLQQVIE
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                                                                                                                                                                       producE="putative prephenate dehydrogenase"
protein_id="BAC74232.1"
db_xref="GI:29610185"
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                                                                                                                   /note="SAV6521"
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                                                   5660. .6754
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                      PheAsnLeuPheAsnGluThrTyrLysSerAlaSerGlnLysHisTrpLysAsnLeuLys 163
                                                                                                                                                        AlaSerSerGlyIleGluThrPheMetArgSerValArgAsnLysLeuGluGluAlaGly 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      335 SerAlaPheArgLeuCysAsnSerLysSerGluGlyIleAsnValGluLeuArglleGly 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          375 ileGluGluLysLeuGluLeuProProProAlaSerGlyAsnValTyrAsnAspLysGlu 394
                                                                                                                                                                                                                                             940 TATGACGATGCGCTCAAGGCGATGATGCAATTTTTGTTAAAAAGGGCATCAAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                236 MetAlaGluGlnSerGlyMetValAlaThrPheMetAlaLysLeuSerSerThrAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1468 TCGCCGGAGCTCGCTCGCCACTCGCGCGCGTCATTGGAGGAGGCTGCCGGCATTTTCCGC
                                                                                      829 AGTTCTTCGGACATC-----ATGGGTGAAGTTCGCAAGTACATGCGTGATGCGGGA
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                                                                                                                                                                                                                                                                                          ProAlaAspProLeuThrMetAlaAspArgHisIleIleAlaLysHisGlyValArgGlu
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Pseudomonas sp. KIE171 species isopropylamine degradation gene cluster (ipuABCDEFGH genes), strain KIE171.
AJ311159 AJ311159.1 GI:15865461
gamma-glutamyl-L-1-hydroxyisopropylamide hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1588 AAAGTTTGGGAGATTAAACAGTCCAATAGTTTCGTGAATAATTGGGAGTTG 1638
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NRTVSHRAITSAGSAARVENRIPGADTNPYLVIAASLLSGLYGIENKLKPKDPILGNA
YKVSPELARPLAASLEEAAGIFRESEMARVIPPNEFVEHYAQMKVWEIKQSNSFVNNW
                                                                                                                  Leisinger, T., van der Ploeg, J., Kiener, A.M., de azevedo Waesch, S.I. and Maire, T. Method för the biotechnological production of 1-alaninol Patent: WO 0173038-A 6 04-OCT-2001; Lonza AG (CH)
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DQWRSINPVEKSGHCYSMLHHSSSSDIMGEVRKYMRDAGIVLEATNSEHGPGQYEINI
                                                                                                                                                                                                                                                                                                                                                                                                                             FLNKAALDGTQISNILFGWDVADHLVDGLEFTGWDSGYPDIALIPDLSTLSLVPWQEK
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ATAGATGGAGTCTGGCGGTAAGCAAGTTGGCGCAGAGTATTTCTTGAATAAGGCGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YTLILIALEAYIGVVLSGTLSSLAGISLPWMLYTIGIVAFVGFLGYRNVBLSAKVLGV
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codon start=1

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4194. .5354
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                    gene; jubu gene; jubE gene; jupE gene; jubu gene; jubu gene; jubu gene; jubu gene; jubu gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE gene; jubE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         de Azevedo Waesch, S.I.
Direct Submission
Submitted (03-MAY-2001) de Azevedo Waesch S.I., Microbiology, Swiss
Federal Institute of Technology Zurich, Schmelzbergstrasse 7, 8092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /producT="putative reductase"
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gamma-glutamylisopropylamide synthetase; ipuA gene; ipuB gene; ipuC
                                                                                                                                                                                                                                                                                                                                                               Kiener, A. and Leisinger, T. Transformation, A., Transformation of isopropylamine to L-alaninol by Pseudomonas sp. strain KIE171 involves N-glutamylated intermediates Appl. Environ. Microbiol. 68 (5), 2368-2375 (2002)
                                                                                                                                                                                                                                                                                                                                                           de Azevedo Wasch, S. I., van der Ploeg, J.R., Maire, T., Lebreton, A.,
                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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gene="ipuC"
function="isopropylamine degradation"
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                                                                                                                                                                                                                                                                                  Pseudomonadaceae; Pseudomonas.
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1. .11355
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transT table=
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transl_table=
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AUTHORS
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TITLE
JOURNAL
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CDS

FEATURES

TITLE

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   3289 AGTTCTTCGGACATC-----ATGGGTGAAGTTCGCAAGTACATGCGTGATGCGGGA 3339
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I (bases I to 128136)
Larbig,K.D., Christmann,A., Johann,A., Klockgether,J., Hartsch,T., Merkl,R., Wiehlmann,L., Fritz,H.J. and Tummler,B.
Gene Islands Integrated into tRNA(Gly) Genes Confer Genome Diversity on a Pseudomonas aeruginosa Clone
J. Bacteriol. 184 (23), 6665-6680 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic sequence, integrated
                                                          3340 ATCGTACTAGAAGGGACGAACAGTGAACACGGCCCTGGCCAGTACGAGATCAACATCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gammaproteobacteria; Pseudomonadales;
                                     196 IleLeuMetGluAlaThrHisProGluPheLeuProSerGlnHisGluLeuAsnPheVal
                                                                                                            216 ProAlaAspProLeuThrMetAlaAspArgHisIleIleAlaLysHisGlyValArgGlu
                                                                                                                                              3400 TATGACGATGCGCTCAAGGCAGCGATGATGCAATTTTTGTTAAAAACGCATCAAGGAA
                                                                                                                                                                                    MetalaGluGlnSerGlyMetValAlaThrPheMetAlaLysLeuSerSerThrAlaLeu
                                                                                                                                                                                                                                                          GlyAsnAlaCysHisIleHisMetSerLeuGlnAsp---AlaGluThrGluLysAsnAla
                                                                                                                                                                                                                                                                               PheTyrAspGlnAsnAspGluTyrGlyMetSerThrLeuAlaArgAsnTrpIleAlaGly
                                                                                                                                                                                                                                                                                                                                                     LeuLeuLysTyrValProGluAlaThrTyrPhePheAlaSerTyrIleAsnSerTyrLys
                                                                                                                                                                                                                                                                                                                                                                                                                                          3634 ATGGTTGCCCTTGCCCGAGAAATGTCGGCCATCTATTTGCCGAATATCAACTCCTACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315 ArgLeuGinProLeuThrPheAlaProThrLysCysCysTrpAlaIleAspAsnArgThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3694 CGGACGGCTGGCGCATCCTGGCCGGCGGTAATTCGTCCTGGGGATTCGACAACCGCACC
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ELGGKEPNI ILASYGDIEKAAVASAESMFNNQGEVCIAPSRLIVERSIHKRVVEIVAE
VAKRRQPGDPLDPTTRMGALVDANHADRVMGFIGRAKADGATLVAGGTRALTETGGSY
VVPTVPDNVSNCMETARABEVGEPVLSVI PVAAVGEAVAVANDSPYGLGAGVMTDRLSD
AHKISRELRAGVVYVNCYNDCDITTPPGGVKQSGNGRDKSLYALDEYTELKTTWIKL"
ARRSESVHAMNTKI APALALVGLVGFLYI AFNNLSALTGSEGYNKVNVTI VVLLI VAF
LVGSGGAVI MKMKA PRRFASI LINHMS"
                                                                                                                                                                                                                                   /translation="MSGDYMYOATTNLVGAAYWRGRADBIOFEGRCLIDGKMVEAQSG
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LIRLHRDELALLETLDMGKPISASRSVDVEAVASCFEWYAEAIDKLYEQIAPTAETDL
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                                                                                                                                                                                                                                                                                            ALITREPLGVVGAIVPWNFPMLTAAWKTAPALACGNSVVLKPAEQSPLTAIRLAQLAI
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    db_xref="GI:15865469"
    db_xref="SPTREMBL:Q93655"
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159
73
194
31
                                                                                                            function="isopropylamine degradation"
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Mismatches:
Indels:
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                                    3051. .9574
/gene="ipuH"
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gene="ipuH"
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50.77%
34.79%
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Query Match:
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MLABWGCEBVQGFFISKPIPGSDFQDWRLSFH"
22070. 24477
/note="insertion sequence of the IS21 family; the
/note="insertion sequence is flanked by inverted repeats and
insertion sequence is flanked by inverted repeats and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAN62255.1"
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20010. .20996
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IRTETEVADLTVPDAASDLGYVLAAVKEIRSALAGRVPLIGFSGSPWTLATYMVEGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (21066. .21818)
/gene="ORF SGS"
/note="originally longer protein; the integration of an IS-element disrupted the CDS (ORFS SGB and SGS)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contains a transposase and a NTP-binding protein; upon insertion into ORF (SG5 and SG8) a sequence of 7 bp (CCTTAGT) was duplicated"
//evidence-not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
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/product="hypothetical protein with methyl-accepting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22083. . 22137
hote-repeats L1 and L2 are inverted with respect
and R2 found in the repeat region at the other end
insertion sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22070. 24477 // Anote="located on the gene island PAGI-3(SG)"
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22077. .22104
/note="terminal IR of insertion sequence"
/rpt_type=inverted
22083. .22137
                                                                                                                                                                                                                                                                                          /transl_table=11 / /product="conserved hypothetical protein"
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22070. .22076
/note="flanks insertion sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain of chemotaxis transducer"
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/db xref="G1:24461657"
                                                                                                                                                                                                                                                                    experimental
                                                                                                        PEVVKVFVDAVHELSKPYH"
                                                                                                                                   19225. .19680
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19225. .19680
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                                                                                                                                                                                                                'gene="ORF SG3"
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20010. .20996
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/gene="ORF SG4"
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evidence=not
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DFLSLCKNRELACEVTLQPLERYDLDAAILFSDILTIPDAMGLGLYFEEGEGPRFKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="bacteriophage P4 integrase subfamily; similar to
Xylella fastidiosa XF1718 (int) and Pseudomonas aeruginosa
C ORF C1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELLRKIRCYRGNI TTQLGIRLLLLTGVRTGELRLATPDQFDLERGLWI I PPEVVKQLQ
DGWRKRGKRPQDI PPYI VPLSVQA I EI VRYLLEQVKPAQRHLLAHRGDLKKR I SENTL
NAALRRMGYEGLLTGHGI RGTLSTGLNEI GYPKI WVDAQLSHADPNKVSATYNHALYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MALTDVAVRQARPTGKDYTLPDFDGLSLAVSAKGGKSWHFRYYW
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VYLOWLAHRRLELKEGROSTLSQIORI FDKDVLPPLGTVTI FDIRRSNLLDVLATIEQ
RGAFTTAEKVRTWFROLFRFAMVKAEGLVGNPASDLDVVAAPKPPVAHNPFLRLHELP
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/product="tRNA-Glu"

15790. .15865

/product="tRNA-Gly"

15842. .15865

/note="att L site; flanks Pseudomonas aeruginosa SG17M

gene island PAGI-3(SG); 24 terminal nucleotides of the 3'
                                                                                                                                                                                                                                                                                                                                                                                                                          1. .15865
/note="corresponding genomic region to Pseudomonas
aeruginosa PAO1 from gene PA2836 to gene PA2820 with an
average nucleotide substitution rate of 0.27%; all
annotated genes are conserved and show only a few amino
     2 (bases 1 to 128136)
Larbig,K.D., Christmann,A., Johann,A., Hartsch,T., Merkl,R.,
Klockgether,J., Fritz,H.-J. and Tuemmler,B.
Direct Submission
Submitted (30-OCT-2001) Klinische Forschergruppe, Medizinische
Hochschule Hannover, Carl-Neuberg-Strasse 1, Hannover 30623,
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15866...119169
/note="Pseudomonas aeruginosa SG17M gene island
PAG1-3 (SG3), integrated into the first Gly-tRNA gene"
15907...15934
/note="AT-rich"
                                                                                                                                                                                                                                                                                                                                                /map="between genes PA2836 and PA2815"
/clone="C"
/note="hypervariable genome region"
                                                                                                                                                                                                                                              organism="Pseudomonas aeruginosa"
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transl_table=11
product="putative integrase"
protein_id="AAN6223.1"
/db_xref="GI:24461654"
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/transl_table=11
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                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
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/db_xref="taxon:287"
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                                                                                                                                                                                          Location/Qualifiers
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16091. .17500
/gene="int"
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/note="ORF SG2"
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/gene="int"
/note-":
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-----TCTAGTTCTTCGGACATC-----ATAGGTGAAGTTCGCAAGTACCATGCGT
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                                                                GluLeuGluPheAsnLeuPheAsnGluThrTyrLysSerAlaSerGlnLysHisTrpLys
                                                                                                                                                                                                                                                                                                                   193 GluAlaGlyIleLeuMetGluAlaThrHisProGluPheLeuProSerGlnHisGluLeu
                                                                                                                                                                                                                                                                                                                                                       33446 GATGCCGGGATCGTACTAGAGGCGACGAGCAGTGAACATGGCCCGGGCCCAGTACGAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 AlaGlyLeuLeuLysTyrValProGluAlaThrTyrPhePheAlaSerTyrIleAsnSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33866 CGCACTGTGTCGCACCGTGCGATCACATCAGCCGGCGGCGGCCGCTCGGGTCGAGAACCGG
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                                                                                                                                                                           33350 AGCATTAATCCAGTGGAAAAGAGTGGCCACTGCTACAGCATGCTCCATCAC
                                                                                                                                             161 AsnLeuLysThrAlaGlnPro--
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32948 ATAGATGGAGTCTGGCGCGGAAGCAAGTCGGAGCAGAGATACTTTCTGAACAAAGCGGCT 33007
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                                                                                                                                                                                                                                                                                                                                                                                                                 RKMFVVAYPRETQEMVLDAHNRAFAFFGGVPQRVIYDNLKTAVDAILVGKDRIFNRF
LALANHYLFEPVACTPAAGWEKGQVENQVGNIREWLFTPLARFASFADLNHWLATRCQ
ELAQRKHPTERSRSTAECFVQEQAHLRVIDAPFDGYVEQMRSVSSTCLVRVDRNQYSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAQWAGKVTSVRCTADEIRIVADDQLIARHARRFGRDQLVYDPWHYLAVLDKKPGALR
NGAPFVTWDLPEPIKQVREYLLKQSRGDRAFVDLLLLARDVGLEALQVACELALESGV
                                                                                                                                                                                                                                                                                                                                                       translation="MISMDIIAEIRRRHLVSGETISVIARSLNLSRPTVRKHLRSTTA
                                                                                                                                                                                                                                                                                                                                                                                              !LVKQWKALKTRPGAAQAFIPLLFAPGEACQFDWSHEQAEIAGVMQTIKVAQFRLCHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein of insertion
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Matches:
Conservative:
Mismatches:
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transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3678. .24421
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595.00
50.98%
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Best Local Similarity:
  repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MISLREHQVEANARIRAWAGFPTRSPVPAQGLRGTVVSATGSGK
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COMD1ement (3433. .3939)
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Direct Submission

Direct Submission

Direct Submission

Submitted (19-MAR-2002) Director-General of Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; 2-49-10 Nishinara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:bio@mite.go.jp, URL:http://www.bio.nite.go.jp/;
This work was done in collaboration with Haruo Ikeda(*1), Jun Ishikawa(*2), Akiharu Hanamoto(*3), Chigusa Takahashi(*3), Mayumi Shinose(*3), Hiroshi Horikawa(*4), Hidekazu Nakazawa(*4), Tadayoshi Osonoe(*4), Norihiro Kushida(*4), Hidekazu Nakazawa(*4), Tadayoshi Shiba (*5), Yoshiyuki Sakaki(*6,*7), Masahira Hattori(*1,*7)

Final finishing process and all annotation were done by H. Ikeda and J. Ishikawa.

*1 Kitasato Institute for Life Sciences, Kitasato University
*2 National Institute for Life Sciences, Kitasato University
*3 The Kitasato Institute for Life Sciences, Kitasato University
*3 The Kitasato Institute for Life Sciences, Kitasato University
*3 The Kitasato Institute for Life Sciences, Kitasato University
*3 The Kitasato Institute for Life Sciences, Kitasato University
*3 The Kitasato Institute for Life Sciences Kitasato University
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Shiba,T., Sakaki,Y., Hattori,M. and Omura,S.
Complete genome sequence and comparative analysis of the industrial
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                                                                                                                                                                                                                                     Omura, S., Ikeda, H., Ishikawa, J., Hanamoto, A., Takahashi, C., Shinose, M., Takahashi, Y., Horikawa, H., Nakasawa, H., Osonoe, T., Kikuchi, H., Shiba, T., Sakaki, Y. and Hattori, M. Genome sequence of an industrial microorganism Streptomyces
                                                            Straptomyces avermitilis MA-4680
Streptomyces avermitilis MA-4680
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 98 (21), 12215-12220 (2001)
21477403
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*7 RIKEN, Genomic Sciences Center
Pollowing url is also available.
http://avermitilis.ls kitasato-u.ac.jp.
Location/Qualifiers
1. 300550
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*5 School of Science, Kitasato University
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Nat. Biotechnol. 21 (5), 526-531 (2003)
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                                                                                                  ORGANISM
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JOURNAL
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                            KEYWORDS
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BAXAPSGRWAHRLUGGHGVDAALLTALDTALSLAANSPAAABALQQLTPSVQELR

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TAMLLDYYPAWEHRRQKGQHSAMGWSQYELLSAICPSRRSDAGGRRTAEWERKFPGQV
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SRARDGEBEREFUDFAFTLGPDAPATYLCAIVGATPHLDADARWEQLALHTHQILGBAA
APTICRALQSARQNFTAASLPALDSYTTDPHBQDIRADABGTRTDLLTAGWNATRG
QAALTVAALLFHGSEHLHALTPLVTRLANDSVLAVRVCAAQAVLALMKHDPQIALDTI
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QMCPRSTVAVLRMLGRVRTAVRAGHAEYTGTAPAQDDVLDLRALGQRSRTPAGI RQPK
CWRLSSSRWLFRVSSSTRSVRCPVSRASSCCPSWRFREHRRTPPDAAVAPWAAQQPP
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transl_table=11

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/protein_id="BAC6717.1"

/db_xref="GI:29603644"
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/note="SAV8"
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transl_table=:
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227991 ACCAAGCTGCCCGGCGGACCGGAGATGTGCGCCTACATCCTGGCGACAGACGTGGACATG 228050
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                                                                                                                                                                                      227871 GTGACACTCGAAGAGCTCGGCCACCTCGTTCAAGGCCGTGAGATCGACACGGTGATGGTC
                                                                                                                                                                IleThrTyrAspGluLeuAsnAsnLeuIleArgAsnGlyLysIleAspThrValValLeu
                                                                                                                                                                                                                               AlaCysValAspMetGlnGlyArgLeuMetGlyLysArgLeuThrGlyArgHisPheLeu
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                                                Conservative:
Mismatches:
Indels:
                 Length:
Matches:
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Query Match:
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421 GluLysLeuIleLeuHisTyrValAsnAlaAlaAsnValGluIleAsnGluPheSerLys 440

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                                                                                                                                                    228111 GTCCCCGACCTGGGCACCCTGAACTACCTGCCAGGCACGGTCCTCGTACAC
                                                                                                                                                                                                                                                               228171 GGCAACGCCGTACA---CCCGACGGCCGCCCCTCGCCGTCGCACCACCACGGGAGATCCTC
                                                                                                                                                                                                                                                                                                                                                                                228288 GAATTCGTCCTCTACAAAGGCACCGAAGCACAGCTGCGCCCGATCCGGGTTCAGGAACCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228527 GCATGCGACACCTCCACAAACACGCCGTCCGTCACATCGCCGCACAACACGC
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                                                     AACCCGCTGGACGGGTTCGAACTCGCCGGCTGGCACACCGGAATACGGAGACCTGCGTGTC
                                                                                                                                                                                                                        SerAsnProHisAsnPheValThrSerGluProLeuPheCysSerProArgValIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluPheAsnLeuPheAsnGluThrTyrLysSerAlaSerGlnLysHisTrpLysAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PheMetArgSerValArgAsnLysLeuGluGluAlaGlyIleLeuMetGluAlaThrHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 ProGluPheLeuProSerGlnHisGluLeuAsnPheValProAlaAsp---ProLeuThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228752 CAGCTGGTTCCGCTGTACGCACCCCACCCCCAACTCCTACAAACGATATGTCCGCCACTCC
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Search completed: December 18, 2003, 00:54:26 Job time : 6869 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 17, 2003, 22:42:10; Search time 19 Seconds
(without alignments)
2297.925 Million cell updates/sec
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Title:

Derfect score: 2376
Sequence:

I MTITYDELNNLIRNGKIDTV.....INEFSKQVTDWELNGFNRY 454
Scoring table: BLOSUN62
Gapop 10.0, Gapext 0.5
Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0 Maximum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database: PIR_76:*
1: pir1:*
2: pir2:*
3: pir2:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

glutamine syntheta probable glnA4 proglutamate-ammonia probable glnA4 propobable glutamine syntheta glutamine syntheta conserved hypothet glutamate-ammonia glutamate-ammonia glutamate-ammonia probable glutamine probable glutamine probable glutamine probable glutamine probable glutamine glutamate-ammonia glutamate-ammonia hypothetical prote glutamine syntheta glutamine syntheta glutamine syntheta glutamine syntheta glutamine syntheta glutamine syntheta glutamate-ammonia glutamate-ammonia glutamine syntheta glutamine syntheta Description SUMMARIES H97616 AI3578 F70885 T36848 C84133 G75517 H86899 B83609 A83391 D83609 A43995 AJBSQS C95058 AF2839 T51803 H89905 AJBSQU AH1599 AC1237 AJCLOA DB Query Match Length 118.0 118.0 118.0 118.2 118.2 118.2 118.3 942.5 942.5 799.5 798.5 510.5 469 465 464.5 464.5 464.5 464.5 485.6 487.5 484.5 487. 480 Result

glutamine syntheta	glucamare-ammonia qlutamate-ammonia	probable glutamine	glutamate-ammonia	glutamine syntheta	probable gln2 - My	glutamine synthase	glutamine syntheta	glutamate-ammonia	glutamine syntheta	glutamine syntheta	glutamine syntheta	glutamine syntheta	probable glutamine	conserved hypothet
AB2600	145/36 T45145	C97382	A64468	F69076	B70776	A87113	C75009	T47127	B84359	E69368	H87636	A36911	D71143	D83449
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460	448	452	454	442	446	448	439	454	454	491	465	439	443	454
16.9	16.9	16.8	16.8	16.6	16.6	16.5	16.4	16.3	16.3	16.2	16.2	16.1	15.8	15.8
401.5	400.5	400	398.5	395	393.5	391.5	389.5	387.5	386.5	386	385.5	381.5	376	375
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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RibelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Golteman, E.; Salkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesse Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 FVMKPDLSTLRLAPWLEKTAIVLCDVLDHH---HDDLSHSPRAVLKKQVQRLHERGYRAY 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSHVHNSIWSADGKEPLFFDPKAPYTMTPLMRSWVAGQIKYATDYTYFLAPYINSYKRFQ 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 CHLCADLNSLHILLPWSEGAVLAISN--PHNFVTSEPLFCSPRVILMQQIERLANLKLKGL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 PASELEFNLFNETYKSASOKHWKNLKTAOPHHOWMNISASSGIETFWRSVRNKLEEAGIL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318 PLTFAPTKCCWAIDNRTSAFRLCNSKSEGINVELRIGGADLNPYLAFSAIIAAGISGIEE 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLELPPPASGNVYNDKELPEPPNSLQNATHLLKESKMLNKTFGEKLILHYVNAANVEINE 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 MEATHPEFLPSQHELNFVPADPLTMADRHIIAKHGVREMAEQSGMVATFMAKLSSTALGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 VLAC-VDMQGRLMGKRLTGRHFLGLDQKKISISTFVYAVTIEGIAGGGYEISSVDTGYSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MLACIVDMQGRLIGKRFYGQFFVESGYDETHGCNYLLADDIDMEPVPGYEAAGWDKGYGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACHIHMSLQDAETEKNAFYDQNDEYGMSTLARNWIAGLLKYVPEATYFFASYINSYKRLQ
                                                                                                                                                                                                         PIDN: AAL53796.1; PID: 917984727;
                                                                                                                                                                                                                                                                                                                                                                                                                                       78; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Score 927; DB 2;
Pred. No. 9e-68;
                                                                                                                                                                                                                                                                                                  A;Map position: II
C;Superfamily: glutamate-ammonia ligase
C;Keywords: ligase
                                                                                                     A; Accession: A1578
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-434 < KUR>
A; Cross-references: (B: AE008918; PIL
A; Experimental source: strain 16M
C; Genetics:
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Best Local Similarity 43.9%;
Matches 192; Conservative 78
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YDRRVTDWELYRGFERY
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                                                                                                                                                                                                                                                                             A, Gene: BMEII0554
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                                                                                                                                                                                                                                              probable glnA4 protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Jo.Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: H97616
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2322-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUD:21608551; PMID:11743194
A;Accession: H97616
A;Accession: H97616
A;Accession: H97616
A;Residues: 1-454 «KUR>
A;Residues: 1-454 «KUR>
A;Cosserreferences: GB:AE007869; PIDN:AAK87889.1; PID:g15157281; GSPDB:GN00169
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glutamate-ammonia ligase (EC 6.3.1.2) [imported] - Brucella melitensis (strain 16M)
c/species: Brucella melitensis
c/spacies: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 AGGGYEISSVDTGYSDCHLCADLNSLHLLPWSEGAVLAISNPHNFVTSEPLFCSPRVILM 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVPGYKSSSWEKGYGDYTLKPDLSTLRKVPWLEGTALVLCDVLDHHTHEEVPHSPRALLK 124
       423
                              364 MAALLAAGIDGIENKLELEPAFVGDAYGKDVREIPKTLRDATAFLDGSKMLRQAFGDDV 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MRALRKGLOGAGIPVENSKGEASPGOAEINVRYAEALTMADRHAIIKNATKEIAWSKGKA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 ATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLARNWIAGLLKYVPEAT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 FSAIIAAGISGIEEKLELPPPASGNVYNDKELPEFPNSLQNATHLLKESKMLNKTFGEKL 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
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       FSAIIAAGISGIEEKLELPPPASGNVYNDKELPEFPNSLQNATHLLKESKMLNKTFGEKL
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39.74; Score 942.5; DB 2;
Best Local Similarity 43.34; Pred. No. 5.2e-69;
Matches 195; Conservative 89; Mismatches 165;
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VDHYVHAARWEQEEYDRRVIDWEVARGFER 453
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A,Map position: circular chromosome
C,Superfamily: glutamate-ammonia ligase
       364
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probable glnA4 protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: F70885
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Comnor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamiln, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
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                                                                                                                                                                                                          178
                                                                                                                                                                                                                                                                                                                                                         184
                                                                                                                                                                                                                                                          GIETFMRSVRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTMADRHIIAKHGVREMAE 238
                                                                                                                                                                                                                                                                                  244
                                                                                                                                                                                                                                                                                                        OSGMVATEMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLARNWIAGLLKY 298
                                                                                                                                                                                                                                                                                                                          LNTVPGYAMASWDTGYGDMVMTPDLSTLRLIPWLPGTALVIAD-LVWADGSEVAVSPRSI 127
                                                                                                                                                                                                                                                                                                                                                                                                         NPYLAFSAIIAAGISGIEEKLELPPPASGNVYNDKELPEFPNSLQNATHLLKESKMLNKT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIAGGGYEISSVDTGYSDCHLCADLNSLHLLPWSEGAVLAISNPHNFVTSEPLFCSPRVI 121
                                                                                                                                                           GIAGGGYEISSVDTGYSDCHLCADLNSLHLLPWSEGAVLAISNPHNFVTSEPLFCSPRVI 121
                                                                                                       77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable glutamine synthetase - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Dace: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000 C;Accession: T3648 R;Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, September 1998 A;Reference number: Z21615 A;Accession: T3648 A;Accession: T3648 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                       LMOQIERLANLKLKGL---FASELEFNLFNETYKSASOKHWKNLKTAQPHHQWMNISASS
                                                                                   Gaps
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                                                                                11;
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                                                            Length 457;
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38.9%; Pred. No. 3.2e-57;
Live 84; Mismatches 177; Indels
                                                                                   Indels
                                                         ; Score 799.5; DB 2;
; Pred. No. 2.6e-57;
88; Mismatches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGEKLILHYVNAANVEINEFSKÖYTÖWELNOGFNR 453
||| :: || :| || || || || FGEDVVAHYLINNARVELAAFNAAVTÖWERIRGFER 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ,Genetics:
,Gene: glnA4
;Superfamily: glutamate-ammonia ligase
A; Experimental source: strain H37Rv
                                                         Query Match 33.6%;
Best Local Similarity 38.7%;
Matches 176; Conservative 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 38.9*
Matches 176; Conservative
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Residues: 1-462 <OLI>
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Cyleanine synthetase BH3867 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: C84133
C;Accession: C84133
C;Accession: C84133
C;Accession: C84133
A;Accession: C84133
A;Accession: C84133
A;Accession: C84133
A;Seterance number: A83650; MuID:20512582; PMID:11058132
A;Accession: C84133
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-455 <STO>
A;Residues: 1-455 <STO>
A;Residues: 1-455 <STO>
A;Residues: 1-455 <STO>
A;Experimental source: strain C-125
C;Genetics: C;Conetics: C 12; 370 311 361 301 421 112 EPLFCSPRVILMQQIERLANLKLKGLFAS---ELEFNLFNETYKSASQKHWKNLKTAQPH 168 169 HOMMNISASSGIETFWRSVRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTMADRHII 228 122 LMQQIERLANLKLKGLFASELEFNLFNETYKSASQKHWKNLKTAQPHHQWMNISASSGIE 181 112 SDFEGDPRNILKKTVER---AKEKGYSISVGPELEFFLFE-----TDEYGLPTKQTQDI 162 229 AKHGVREMAEQSGMVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLA 288 289 RNWIAGLLKYVPEATYFFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCNSKSEGIN 348 26 257 MSLTFWAKYNELE-GNSCHIHLSLADAD-GRNAMAEGG---GMSDVWRHFLAGQLVALRE 137 LRRQLERLAGHGYTAQVGTELEFIVFRDTYEHAWDANYRGLTPANQYNVDYSVLGTGRVE MVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLARNWIAGLLKYVPE 312 FSLLYAPHINSYKRFQPGSFAPTAVAWGHDNRTCALRVV-GHGRSLRFENRLPGGDVNPY 66 GG--YEISSVDTGY-----SDCHLCADLNSLHLLPW-----SEGAVL-AISNPHNFVTS 57 GKIMFDGSSI-TGFTPINOSDLYLOPDLTTFAVLPWTEEEGYSEGRFLCSVKKP----DG 223 YKWVVXTVAKQFGLHATFMPKPLGGANGSGMHTNISLFDDEKQENAFYDESDKLGLSKTA 182 TFMRSVRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTMADRHIIAKHGVREMAEQSG 302 ATYFFASYINSYKRLOPLTFAPTKCCWAIDNRTSAFRLCNSKSEGINVELRIGGADLNPY LAFSAIIAAGISGIEEKLELPPPASGNVYNDKELPEFPNSLQNATHLLKESKMLNKTFGE 6 DELNNLIRNGKIDTVVLACVDMQGRLMGKRLTGRHFLGLDQKKISISTFVYAVTIEGIAG -----VTAEQIDSVVD 21.5%; Score blues, -33; 31.1%; Pred. No. 1.1e-33; Five 77; Mismatches 187; Indels 57; 16 EEIKETIKTKOVELLHLQFVDIEGIL--KHVT----::: || | | ||:: | |||||| || EVVAHYRNMARVELDAFDAAVTDWELRRSFER 461 KLILHYVNAANVEINEFSKQVTDWELNQGFNR 453 A,Gene: BH3867 C,Superfamily: glutamate-ammonia ligase Query Match 21.55
Best Local Similarity 31.15
Matches 145; Conservative

셤 ò 셤

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Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, L. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patholy. A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                    A;Accession: C83225
A;Status: preliminary
A;Molecule type: A;Bratus: Dreliminary
A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule
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Nylternate names: glutamine synthetase
C;Species: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 03-Jun-2002
C;Accession: A28676; 811994
R;Janssen, P.J.; Jones, W.A.; Jones, D.T.; Woods, D.R.
B;Acteriol. 170, 400-408, 1988
A;Title: Molecular analysis and regulation of the glnA gene of the gram-positive anaero;
A;Reference number: A28676; MUID:88086901; PMID:2891680
A;Accession: A28676
A;Molecule type: DNA
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A;Cross-references: GB:X55158
A;Cross-references: GB:X55158
Mods, D.T.; Woods, D.R.
Mod. Microbiol. 4, 1575-1583, 1990
A;Title: Studies on Clostridium acetobutylicum glnA promoters and antisense RNA.
A;Reference number: S11994; MUID:91141310; PMID:1981087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        342 SPA---IQGEFEVPEELTLPCTMYDALRRLKGSALARELFGSEFVEGYVATKSMELTSFF 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----NETYKSASQKHWKNLKTAQPHHQWMNISASSGIETFMRSVRNKLBEAGILMEATH 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 PEFLPSQHELNFVPADPLTMADRHIIAKHGVREMAEQSGMVATFMAKLSSTALGNACHIH 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 HEMGTSQFEINFLHGDPVLLADQTFLFKHLLKEVALKHGLIVVCMAKPLAKTPGSSMHIH 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 EGAVLAISNPHNFVTSE-----PLFCSPRVILMQQIERLANLKLKGLFASELEFNLF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 LTGRHFLGLDQKKISISTFVYAVTIEGIAGGGYEISSVDTGYSDCHLCADLNSLHLLPWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 469; DB 2;
Pred. No. 2.3e-30;
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28.8%;
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Best Local Similarity 28.89
Matches 123; Conservative
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399 DEISPWE 405
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on, D.;
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A/Molecule type: DNA
A/Residues: 1-439 <ARN>
A/Cross-references: GB:AE001758; GB:AE000512; NID:g4981480; PIDN:AAD36024.1; PID:g498148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 399, 323-329, 1999
A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A,Reference number: A72200; MUID:99287316; PMID:10360571
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                                                                                                                                                                                                                                                                                                                                                                                                        glutamine synthetase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Species: 11.-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: B72313
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicl
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||IKHAKALAAVTNPTINSYKRLVPGYEAPVYISWSVGNRSALIRIPKARGKATRLEYRSP 333
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401
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                                          SASSGIETFMRSVRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTMADRHIIAKHGVR
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C.fgentelics:
A.fgene: TW0943
C.Superfamily: glutamate-ammonia ligase
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Best Local Similarity
Matches 138; Conserv
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A; Status: prelimina:
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                                                                                       C;Comment: This enzyme catalyzes the formation of glutamine from ammonia and glutamic ac C;Genetics:
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, T.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
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AB3575
Glutamate-ammonia ligase (EC 6.3.1.2) [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LMQQIERLANLKLKGL----FASELEFNLFNETYKSASQKHWKNLKTAQPHHQMMNISA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSGIETFMRSVRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTMADRHIIAKHGVREM 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 AGGGYEISSVDTGYSDCHLCADLNSLHLLPW--SEGAVLAISNPHNFVTSEPLFCSPRVI 121
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                                                                                                                                                                                                                                                                                19.6%; Score 466; DB 1; Length 443
28.0%; Pred. No. 4.5e-30;
iive 84; Mismatches 211; Indels
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28.7%; Pred. No. 6.1e-30;
iive 71; Mismatches 208; Indels
                                                                                                                                                 A;Gene: glnA
C;Superfamily: glutamate-ammonia ligase
C;Keywords: ligase
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C,Superfamily: glutamate-ammonia ligase
C,Keywords: ligase
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Best Local Similarity 28.0%
Matches 130; Conservative
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Best Local Similarity 28.73
Matches 133; Conservative
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Residues: 1-476 < KUR>
A; Status: preliminary A; Molecule type: DNA A; Residues: 1-38 <JA2>
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J.D.; Dodson, R.J.;
T.; Zalewski, C.; M
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A;Accession: G75517
A;Cession: G75517
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-449 < MHIX-A
A;Cross-references: GB:AR001904; GB:AE000513; NID:g6458129; PIDN:AAF10028.1; PID::A;Experimental source: strain R1
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61
                                                                                                85
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C;Species: Deinococcus radiodurans
C;Accession: G7517
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dc, M.; Shen, M.; Vamathevan, J.C.; Fraser, C.M.
S; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                        28 VKNWKQATEWIAWRDIEDIECITPDQAGVARGKMMPSKKF--TSNTSLALPSAVFMTTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | | | | : | | | : | | | | : | | | | : | | | | : | | | | : | | | : | | | | : | : | | | | : | : | | | : | : | | | : | : | | | : | : | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
-CV--DMQGRLMGKRLTGRHFLGLDQKKISISTFVYAVTIE
                                                                                                                                                                                                                                                                                                                 86 GAYPEDGYGFHYPEDD----GDLKLLPDLTTLSAVPWETDSTAQVICDLVYQDGRAVEFTP
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A;Map position: 1
C;Superfamily: glutamate-ammonia ligase
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30.9%;
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Matches 126; Conservative
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1. 明天、聖時

M.J.; B: K.; Lim,

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A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83609
                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-458 <STO>
A;Cross-references: GB:AE004467; GB:AE004091; NID:g99461133; PIDN:AAG03685.1; GSPDB:GN001
A;Experimental source: strain PAO1
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probable glutamine synthetase PA2040 [imported] - Pseudomonas aeruginosa (strain PAO1)
probable glutamine synthetase PA2040 [imported] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa PA01, Hickey, M.J.; B)
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; B)
adman, S.; Vian, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim.,
i. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic paths
                                                                                             probable glutamine synthetase PA0296 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                               C;Species: Pseudomonás aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 15-Jun-2001
C;Accession: B83609
R;Stover. C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J. Lory, S.; Olson, M.V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 DAD-----RICYPIPGTLSMEPWQKRPTAQLLMTMHELEGEPPFADPREVLRQVVARFT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 NLKLKGLFASELEFNLFN-ETYKSASOKHWKNLKTAOPHHOWMNISASSGIETFMRSVRN 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 KLEEA---GILMEATHPEFLPSQHELNFVPA-DPLTMADRHIIAKHGVREMAEQSGMVAT
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HNAVKALPEDTIVTEALGEHVLVNFVEAKRIEWASYAQFVSQWEIDNYLELY 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
19.3%; Score 459; DB 2; Length 45
Best Local Similarity 28.4%; Pred. No. 1.8e-29;
Matches 126; Conservative 82; Mismatches 213; Indels
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C,Superfamily: glutamate-ammonia ligase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99
                                                                             RNWIAGLLKYVPEATYFFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCNSKSEGIN
                                                                                                                                                          349 VELRIGGADLNPYLAFSAIIAAGISGIEEKLELPPPASGNVY-----NDKELPEFPNS
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| SFIAGLLKHAYNFTAITNPTVNSYKRLVPGYEAPVYVAWAGRNRSPLIRVPASRGLSTRV
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  KHGVREMAEQSGWVATFMAKLSSTALGNACHIHMSL-QDAETEKNAFYDQNDEYGMSTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MTITYDELNNLIRNGKIDTVVLACVDMQGRLMGKRL--TGRHFLGLDQKKISISTFVYAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTITAADIRRDVKEKDIKFLRLMFTDILGTLKNVEVPATDEQLDKLFENKMMFD----GS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
                                                                                                                                                                                                                                                           Length 446;
                                                                                                                                                                                                                                     LONATHLLKESKMLNKTFGEKLILHYVNAANVEINEFSKQVTDWELNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.5%; Score 464; DB 2; Length 446 ilarity 29.0%; Pred. No. 6.7e-30; Conservative 80; Mismatches 211; Indels
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Best Local Similarity
Matches 137; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59
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170 RQSFSIDAANEFDPLFEDMYDWCEAQGLDLDTLIHEEGTAQMEINFRHGDALDLADQILV 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                    230 FKRTWREAALKHNVAATFWAKPMTGEPGSAMHLHQSIVDVKTGKNIF--SNADGTWSELF 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289 RNWIAGLLKYVPEATYFFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCNSKSEGIN 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | | : : | | | | | | | | | 348 VENRLAGADANPYLALAASLLCGYIGMVEGIKPSAQVKGRGYERRNL-RLPLTIEAALER 406
                                                                                                                       EGIAGGGYEISSVDTGYSDCHLCADLNSLHLLPWS-EGAVLAISNPHNFVTSEPLFCSPR 119
                                                                                                                                                                                                                  120 VILMQQIERLANLKLKGLFASELEFNLFNET-----YKSASQKHWKNLKTAQPH 168
                                                                                                                                                                                                                                                                                                              HOWMNISASSGIETFWRSVRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTMADRHII 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349 VELRIGGADLNPYLAFSAIIAAGISGIEEKLELPPPASGNVYNDKELPEFPNSLQNATHL 408
                                                             1 MTITYDELNNLIRNGKIDTVVLACVDMQGRLMGKRLTGRHFLGLDQKKISISTFVYAVTI
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                                                                    A Molecule type: DNA,
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A;Reaidues: 1-458 csTO-
A;Reaidues: 1-458 csTO-
A;Cross-references: GB:AE004630; GB:AE004091; NID:g9948041; PIDN:AAG05428.1; GSPDB:GN001
A;Experimental source: strain PAO1
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA2040
C;Superfamily: glutamate-ammonia ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho; Reference number: A82950; MUD:20437337; PMID:10984043
Accession: B83609
Status: preliminary
Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M.J.; Br
K.; Lim,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable glutamine synthetase PA0298 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 24-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, ..., Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 FASYINSYKRLOPLTFAPTKCCWAIDNRTSAFRLCNSKSEGINVELRIGGADLNPYLAFS 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 DAD-----RICYPIPGTLSMEPWQKRPTAQLLMTMHELEGEPFFADPREVLRQVVARFT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 NLKLKGLFASELEFNLFN-ETYKSASQKHWKNLKTAQPHHQWMNISASSGIETFMRSVRN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 KLEEA---GILMEATHPEFLPSQHELNF-VPADPLTMADRHIIAKHGVREMAEQSGMVAT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LCPNVNSYRRFGSQFYVPNAPSWGLDNRTVALRVPTGSPDAVRLEHRVAGADANPYLLLA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366 AIIAAGISGIEEKLELPPPASGNVYNDKELPEFPNSLQNATHLLKESKMLNKTFGEKLIL 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 KIDTVVLACVDMOGRLMGKRLTGRHFLGLDQKKISISTFVYAVTIEG----IAGGGYEIS
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Best Local Similarity 28.4%; Pred. No. 9.5e-29;
Matches 130; Conservative 80; Mismatches 222; Indels 26;
                                                                                                                                                                                                                                                                Length 458;
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A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83391
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C,Superfamily: glutamate-ammonia ligase
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Best Local Similarity 28.2%;
Matches 125; Conservative 8
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                        Accession: A83391
Status: preliminary
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RESULT 1
                                                                                                        December 17, 2003, 22:40:45; Search time 38 Seconds (without alignments) 3083.050 Million cell updates/sec
                                                                                                                                                                                  US-10-098-602A-2
2376
1 MTITYDELNNLIRNGKIDTV......INEFSKQVTDWELNQGFNRY 454
                                                                                                                                                                                                                                                                                                                                                                830525
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                      830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fung:*
1: sp_invertebrate:*
: sp_mammal:*
: sp_mto:*
                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
sp_rvirus:*
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Maximum DB seq length: 200000000
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sp_rodent:*
sp_virus:*
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                                                                                                                                                                                  Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                            Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	O98h15 rhizobium l	Osfwu3 brucella su	Q92ni9 rhizobium m		O8ych5 brucella me	033342 mycobacteri	O88070 streptomyce	Q936t0 pseudomonas	O8qpy7 pseudomonas	O9k665 bacillus ha	Q9ael4 corynebacte	Q8nnh4 corynebacte	Q8fnl7 corynebacte	O9hyp0 pseudomonas	Q8ycks brucella me	Q8fvq7 brucella su
	Q98H15	QBFVU3	Q92NI9	QBUDI3	Q8YCH5	033342	088070	Q936T0	Q8GPY7	Q9K665	Q9AEL4	Q8NNH4	Q8FNL7	Q9HYP0	QBYCK5	Q8FVQ7
DB	16	16	16	16	16	16	16	7	7	16	7	16	16	16	16	16
* Nuery Watch Length DB	465	455	454	454	434	457	462	459	460	455	427	446	516	413	476	476
% Query Match	42.7	40.8	40.5	39.7	39.0	33.6	33.6	25.9	25.0	21.5	19.8	19.8	19.8	19.7	19.6	19.6
Score	1015	969.5	963	942.5	927	799.5	798.5	614.5	595	510.5	470.5	470.5	470.5	469	465	465
Result. No.	1	7	٣	4	ស	9	7	80	თ	10	11	12	13	14	15	16

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deino	psend	psend	_			_	rhizobium	metha	sulfo	therm	xanth	ocean	rhizo	metha	strep	shewa	metha	rhizobium	strep	strep	strep	sulfo	therm	strep	strep	bacil	rhizobium	strep
09rx64	Q91635	091275	089483	Q8p897	O8dvu9	091633	092ry1	Q8py99	0976n5	Q9hi49	Q8pjq2	Q8eqp3	Q92mv2	08tyg1	Q8dxt3	Q8ehf4	Q8tid7	Q98em0	099y41	Q8nzg4	Q8e3£3	097vq9	0977z8	097886	Q8dqx6	Q9kac9	098828	Q9rds6
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09RX6	091635	091275	Q8G4S3	Q8P897	QBDVU9	091673	Q92RY1	Q8PY99	0976N5	Q9HI49	Q8PJQ2	Q8EQP3	Q92MV2	Q8TYG1	Q8DXT3	Q8EHF4	Q8TID7	Q98EM0	Q99Y41	Q8NZG4	Q8E3F3	697769	0977Z8	097586	9ход80	Q9KAC9	Q988Z8	Q9RDS6
16	16	16	16	16	16	16	16	17	17	17	16	16	.91	17.	16	16	17	16	16	16	16	17	17	16	16	16	16	16
449	458	458	445	461	448	452	478	447	483	448	461	445	455	491	448	451	447	456	448	448	448	429	462	448	448	449	478	453
19.5	19.3	19.3	19.1	19.1	19.0	18.9	18.9	18.9	18.9	18.9	18.9	18.8	18.8	18.8	18.7	18.7	18.7	18.6	18.6	18.6	18.5	18.3	18.3	18.2	18.2	18.1	18.1	17.9
464.5	459	458	453	453	451	450	450	449.5	449.5	449	449	447.5	447.5	446.5	445	445	444.5	442	441	441	440	434.5	434	432	432	430	430	425.5
17 ,	18	19	20	21	22	23	24	25	79	27	88	7 62	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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242 GKCITFMAKYDYARAGSSSHVHNSIWSADGKEPLFFDPKAPYTMTPLMRSWVAGQIKYAT 301
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Boistard P., Becker A., Boutry M., Cadieu B., Dreano S., Gloux S.,
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
"Analysis of the chromosome sequence of the legume symbiont
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).
BMBL, ALSP1909, CAC46792.1;
InterPro; IPR001637; GlaA adenyltn.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 19, Last annotation update)
11-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein R02213.
R02213 OR SMC01594.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium.
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SEQUENCE 454 AA; 51112 MW; B4265B789114D431 CRC64;
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; Pred. No. 2.1e-71;
87; Mismatches 168;
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PD001057; GlnA adenyltn; 1.
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135 KQVKRLSERGYIGYFASELEFYLFNETYDSARKKHWQGLDTASPYIGDYQIGITTKEEGV 194
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NCBL_TaxID=29461;
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SEQUENCE 455 AA
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Complete proteome.
SEQUENCE 454 AA.
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MEDLINE=21608551; PubMed=11743194;
MEDLINE=21608551; PubMed=11743194;
Mocolder B., Hinkle G., Gattung Y., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Mollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Mollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
Genome sequence of the plant pathogen and biotechnology agent
Genome sequence of the plant pathogen and biotechnology agent
Science 294.2323-2328(2001)
BEMBL, AEGO09164; AAL4313.1;
REMBL, AEGO09164; AAL4313.1;
RICEPPO: IPRO01637; GlnA adenyltn.
InterPro: IPRO01637; GlnA adenyltn.
REMBL, PEO0120; gln-synt.; I.
REPEMB. PF00120; gln-synt.; I.
                                                                                                                                                                                                                                                           241 GKAITFLAKWNYSAAGSSSHIHQSLWSKDGETPLFFDKNGQYGMSELMRHYVAGQLAHAS
                                                                                                                                                                                                                                                                                                                                                                       GMVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLARNWIAGLLKYVP
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                                                                                                               ETFMRSVRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTMADRHIIAKHGVREMAEOS
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
01-JUN-2003—(TrEMBLrel. 23, Last annotation update)
03. Last annotation update)
03. Calutanine syntherases
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05. Calutanine syntherases
06. Calutanine syn
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ProDom; PD001057; GlnA_adenyltn; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 294:2317-2323(2001).
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MEDLINE=20020109; PubMed=11756688;
MEDLINE=20020109; PubMed=11756688;
MEDLINE=20020109; PubMed=11756688;
MEDLINE=20020109; PubMed=11756688;
MEDLINE=20020109; Mujer C., Los T.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov E., Blzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
The genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
                                                                                                                                                                                                                                  65 TVPGYKSSSWEKGYGDYTLKPDLSTLRKVPWLECTALVLCDVLDHHTHEEVPHSPRALLK
                                                                                                                                                                                                                                                                                                                                                                                                     244 ATEMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLARNWIAGLLKYVPEAT
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                                                                                                                       4 TYDELNNLIRNGKIDTVVLACVDMQGRLMGKRLTGRHFLGLDQKKISISTFVYAVTIEGI
                                                                                                                                                              5 TFDALKMDVAEGRIDTVLACLVDMQGRLMGKRFQAEFFVESAFEETHSCNYVLATDMEME
                                                                                                                                                                                                            64 AGGGYEISSVDTGYSDCHLCADLNSLHLLPWSEGAVLAISNPHNFVTSEPLFCSPRVILM
                                                                                                                                                                                                                                                                                           124 QQIERLANLKLKGLFASELEFNLFNETYKSASQKHWKNLKTAQPHHQWMNISASSGIETF
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                                                                                    Gaps
                                                                                  1;
                                       Length 454;
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Brucellaceae; Brucella.
                                                                                89; Mismatches 165; Indels
50703 MW; 559465BB5613E37E CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT_2002 (TrEMBLrel--22, Last annotation update)
(Glucamine_synthetase ((BC.673,122))
                                       Score 942.5; DB 1
Pred. No. 1.1e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002)
EMBL, AE009691, AAL53796.1; -
InterPro, IPR001637; GlnA_adenyltn.
InterPro, IPR001691; GLN_synth.
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Pfam; PF03951; gln-synt; l.
Probom; PB001057; gln-synt_N; l.
Probom; PB001057; GlnA adenylun; l.
Ligaes; Complete proteome.
SEQUENCE 434 AA; 49582 MW; 1114F
                                     39.7%;
                                                                                Matches 195; Conservative
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  454 AA;
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                                                          Similarity
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299 VPEATYFFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCNSKSEGINVELRIGGADL 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 QHGKSLIFFMAKYDERE-GNSCHIHVSLRGTDGSA-VFADSNGPHGMSSMFRSFVAGQLAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 LAWIELERLVAAGDVDTVIVAFTDMQGRLAGKRISGRHFVDDIATRGVECCSYLLAVDVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 GIAGGGYEISSVDTGYSDCHLCADLNSLHLLPWSEGAVLAISNPHNFVTSEPLFCSPRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                          L-GLUTAMATE + NH(3) = ADP + GLUTAMINE
                  comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                  .5; DB 16; Length 457;
8e-58;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                  GLUTAMINE SYNTHETASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                        88; Mismatches 180; Indels
                                                        databases.
                                                                                                                                                                                                                                                                            Pfam; PF00120; gln-synt; 1.

Pfam; PF03951; gln-synt N; 1.

Probom; PD001057; GlnA adenyltn; 1.

Hypothetical protein; ligase; Complete proteome.

REQUENCE 457 AA; 49747 MW; 735F57E27C615F23 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
101-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative glutamine synthetase (EC 6.3.1.2).
SCO1613 OR SCI35.35C.
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                                       laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ
-!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 799.5;
Pred. No. 8e-
                                                                                                                                                                                             TIGR; MT2928; -.
TubercuList; Rv2860c; -.
InterPro; IPR001637; GlnA_adenyltn.
InterPro; IPR001691; Gln synth.
                                                                                             ORTHOPHOSPHATE.
-!- SIMILARITY: BELONGS TO THE BEMBL; ALO08883; CAA15522.1; -- EMBL; AE007117; AAK47253.1; -- HSSP; PO6201; ILGR.
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38.7%;
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Matches 176; Conservative
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STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodoon R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              SHVHNSIWSADGKEPLFFDPKAPYTWTPLMRSWVAGQIKYATDYTYFLAPYINSYKRFQ
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                                                                                                 VLAC-VDMQGRLMGKRLTGRHFLGLDQKKISISTFVYAVTIEGIAGGYEISSVDTGYSD
                                                                                                                        FVMKPDLSTLRLAPWLEKTAIVLCDVLDHH---HDDLSHSPRAVLKKOVQRLHERGYRAY
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"Deciphering the biology of Mycobacterium tuberculosis from the
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical 49.7 Kab protein (Glutamine synthetase, putative)
GLNA4 OR RV2860C OR MIV003.06C OR MT2928.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773;
                    Length 434;
                39.0%; Score 927; DB 16; Length 4
43.9%; Pred. No. 1.9e-68;
ive 78; Mismatches 161; Indels
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Nature 393:537-544(1998).
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                                                          Matches 192; Conservative
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Nature 417:141-147(2002).
-!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) = ADP + PHOSPHATE
                                                                                                                                                                                                                                                                           physical map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                         Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
Ka set of ordered cosmids and a detailed genetic and physical mithe 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 798.5; DB 16; Length 462; Pred. No. 9.9e-58; Mismatches 177; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TO THE GLUTAMINE SYNTHETASE FAMILY
                     to the EMBL/GenBank/DDBJ databases.
                                                                                                    B.G., Rajandream M.A.;
to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR01691; GlN synth.
PF00120; gln-synt; l.
ProDom; PD001057; GlnA_adenyltn; l.
                                                                                                                                                                                                            MEDLINE=97000351; PubMed=8843436;
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38.9%;
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EMBL; AL939109; CAA20824.1;
HSSP; P06201; 1LGR.
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Oliver K., Harris D.;
Submitted (SEP-1998)
                                                                                STRAIN=A3(2);
Parkhill J., Barrell
Submitted (SEP-1998)
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                                                          SEQUENCE FROM N.A.
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STRAIN=A3(2)
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240 IAAKHGMTATFWAKPSAEWSGSSGHVHMSLSDLAGTP--VPANPENPGALSEVGYNFLAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGGYEISSVDTGYSDCHLCADLNSLHLLPWSEGAVLAISNPHNFVTSEPLFCSPRVILM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 MVALAREMSAIYLPNINSYKRTAGASWAGGNSSWGFDNRTVSHRAITSAGSAARVENRIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              de Azevedo Waesch S.I., van der Ploeg J.R., Kiener A., Leisinger T.; "Degradation of isopropylamine by Beaudomonias speciaes KIE171."; submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
-i- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) = ADP + PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                               (Glutamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=159091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY. EMBL, AJ311159; CAC81335.1; -1 HSSP; P06201; 2GLS. InterPro; IPR001637; GlnA adenyltn. InterPro; IPR001691; GLN Synth. PFam; PF00120; gln-synt, 1. Pfam; PF00120; gln-synt, 1. Pfam; PF03951; gln-synt, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;; Score 614.5; DB 2; Length
;; Pred. No. 1.9e-42;
73; Mismatches 194; Indels
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                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 23, Last annotation update)
Gamma-glutamylisopropylamide synthetase (EC 6.3.1.2)
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                                                                                                                        ::: || || || :: | | || :: | 430 EVVAHYRNMARVELDAFDAAVTDWELRRSFER
                                                                                      422 KLILHYVNAANVEINEFSKOVTDWELNOGFNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthetase) (Glutamate--ammonia ligase).
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ProDom; PD001057; GlnA_adenyltn; 1.
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"Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-433 (2000).
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-!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
EMBL, AP001520; BAB07586.1; -.
                                                                Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                 Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R.
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        455 AA; 50463 MW; BB669371A49325F0 CRC64;
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00120; gln.synt; 1.
Pfam; PF03951; gln.synt, N; 1.
ProDom; PD001057; GlnA adenyltn; 1.
TIGRAMS; TIGR00653; GlnA; 1.
PROSITE; PS00180; GLNA 1; 1.
PROSITE; PS00181; GLNA ATP; 1.
                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                                                HSSP: P06201; ILGR.
InterPro; IPR001637; GlnA.
InterPro; IPR001637; GlnA.
InterPro; IPR001637; GlnA.
InterPro; IPR001691; GLN.
Synth.
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22,
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Matches 145; Conservative
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01-OCT-2002 (TrEMBLrel.
                                                                  Firmicutes;
                 Glutamine synthetase
                                                 Bacillus halodurans
                                                                                NCBI_TaxID=86665;
                                                                                                                                                                                                  Horikoshi K.,
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Q9AEL4
ID Q9AEL
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                                                                                                                                                                                                                                                                                                                                STRAIN=SG17M;
MEDLINE=22313472; PubMed=12426355;
Larbig K.D., Christmann A., Johann A., Klockgether J., Hartsch T.,
Larbig K.D., Christmann L., Fritz H.J., Tummler B.;
"Gene Islands Integrated into tRNA(Gly) Genes Confer Genome Diversity
on a Pseudomonas aeruginosa Clone.";
J. Bacteriol. 184:6665-6680 (2002).
EMBL; AF440524; AAN62237.1;
SEQUENCE 460 AA; 50620 MW; 35FD0D472764D446 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGLLKYVPEATYFFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCNSKSEGINVELR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.0%; Score 595; DB 2; Length 460; 33.6%; Pred. No. 7.8e-41; Live 80; Mismatches 191; Indels
                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
   447
                     ||:| : | : : | | : : | | ESEMARVIFUNNWEL 452
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 ESKMLNKTFGEKLILHYVNAANVEINEFSKOVTDWEL
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Q9K665;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 154; Conserv
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                    NCBI_TaxID=287;
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                                 416
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   411
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                                                                                    RESULT 9
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DB 16; Length 455;

57 GKIMFDGSSI-TGFTPINQSDLYLQPDLTTFAVLPWTEEGYSEGRFLCSVKKP----DG 111 112 EPLFCSPRVILMOQIERLANLKLKGLFAS---ELEFNLFNETYKSASOKHWKNLKTAOPH 168 112 SDFEGDPRNILKKTVER----AKEKĞYSISVGPELEFFLFR-----TDEYGLPTKQTQDI 162 169 HQWMNISASSGIETFMRSVRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTMADRHII 228 223 YKWVVKTVAKQPGLHATFMPKPLGGANGSGMHTNISLFDDEKQENAFYDESDKLGLSKTA 282 289 RNWIAGLLKYVPEATYFFASYINSYKRLOPLTFAPTKCCWAIDNRTSAFRLCNSKSEGIN 348 349 VELRIGGADLINPYLAFSAIIAAGISGIEEKLELPPPASGNVYN-----DKELPEFPNS 401 6 DELINNLIRNGKIDTVVLACVDMQGRLMGKRLTGRHFLGLDQKKISISTFVYAVTIEGIAG 16 EEIKETIKTKAVELLHLQFVDIEGIL--KHVT-2------VTAEQIDSVVD 229 AKHGVREMAEQSGMVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLA 66 GG--YEISSVDTGY----SDCHLCADLNSLHLLPW-----SEGAVL-AISNPHNFVTS Gapa 57; Indels 402 LONATHLLKESKMLNKTFGEKLILHYVNAANVEINEFSKQVTDWEL 21.5%; Score 510.5; DB 16; 31.1%; Pred. No. 8.1e-34; ive 77; Mismatches 187; Ą 427

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| :| :| :| :| | T----IARPDPSTFQVLPLEAGISKLQAARLFCDVTMPDGQPSFSDPRQVLRRQVQLAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 NLKLKGLFASELEFNLFNETYKSASQKHWKNLKT-----AQPHHQWMNISASSGIETFM 184
                                                                                                                                                                                                       "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO03281; BAB96622.1; -.
InterPro; IPR001691; GlnA_adenyltn.
InterPro; IPR001691; GLN_anth.
Pfam; PF00120; gln-synt; 1.
Propom; PF00150; gln-synt N; 1.
Probom; PD001057; GlnA_adenyltn; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 GKIDTVVLACVDMQGRLMGKRLTGRHFLGLDQKKISISTFVYAVTIEGIAGGGYEISSVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GHLKSWWAPAELESAL-----EEGIGFD------GSAIEGYA----RISEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 TGYSDCHLCADLNSLHLLPWSEG-AVLAISNPHNFVT---SEPLFCSPRVILMQQIERLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 RSVRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTMADRHIIAKHGVREMAEQSGMVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 TFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEYGMSTLARNWIAGLLKYVPEATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 FFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCN---SKSEGINVELRIGGADLNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 VINQWVNSYKRIVYGNEAPTAATWGVSNRSALVRVPTYRLNKBESRRVEVRLPDTACNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---YNDKELPEFPNSLONATHLL
                                                                            Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium efficiens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                               84; Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KESKMLNKTFGEKLILHYVNAANVEINEFSKQVTDWELNQGFN 452
                                                                                                                                                                                                                                                                                                                                                                446 AA; 50381 MW; 30E54AC65E3B2CF1 CRC64;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Glutamine synthase (EC 6.3.1.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
6.3.1.2).
                                                                                                                                                                                                                                                                                                                                                                                                 DB 16;
                                                                                                                                                                                                                                                                                                                                                                                               Score 470.5; DB 10
Pred. No. 1.6e-30;
                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAFSAIIAAGISGIEEKLELPPPASGNV----
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28.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glutamine synthetase II
GLNA2 OR CE2127.
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                Nakagawa S.;
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                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 NLKLKGLFASELEFNLFNETYKSASQKHWKNLKT-----AQPHHQWMNISASSGIETFM 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 VTNQWVNSYKRIVYGNEAPTAATWGVSNRSALVRVPTYRLNKEESRRVEVRLPDTACNPY 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAFSAIIAAGISGIEEKLELPPPASGNV------YNDKELPEFPNSLQNATHLL 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGYSDCHLCADLNSLHLLPWSEG-AVLAISNPHNFVT---SEPLFCSPRVILMQQIERLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 GKIDTVVLACVDMQGRLMGKRLTGRHFLGLDQKKISISTFVYAVTIEGIAGGGYEISSVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSVRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTMADRHIJAKHGVREMAEQSGMVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 FFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCN---SKSEGINVELRIGGADLNPY
                                                                                                                                                                                                                          MEDLINE=21338478; PubMed=11445173;
Nolden L., Farwick M., Kraemer R., Burkovski A.;
"Glutamine synthetases of Corynebacterium glutamicum: transcriptional control and regulation of activity.";
FEMS Microbiol. Lett. 201:91-98(2001).
-!- CATALVITY: ATP + L-GLUTAMATE + NH(3) = ADP + PHOSPHATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 427;
                                                                                                             Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY:
BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
BENBL, AJ310086; CAC34378.1; --
HSSP; P06201; ILGR.
INTERPRO; IPR001637; GlnA adenyltn.
InterPro; IPR001637; GlnA synth.
Pfam; PP00120; gln-synt; I.
Pfam; PF003951; gln-synt; N; I.
ProDom; PD001057; GlnA_adenyltn; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::|::: | | : :: || : : EKSELVADILGEHVFEFFLRNKWREWRDYQEQITPWELRNNLD 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KESKMLNKTFGEKLILHYVNAANVEINEFSKQVTDWELNQGFN 452
             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-GCT-2002 (TrEMBLrel. 22, Last annotation update)
Glutamine synthetase 2 (EC 6.3.1.2) (Glutamate--ammonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              427 AA; 48146 MW; CE5326A81A2406F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.8%; Score 470.5; DB 2; 28.9%; Pred. No. 1.5e-30; ative 84; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 28.94
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                             L-GLUTAMINE.
                                                                                                                                                            NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ligase.
SEQUENCE
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QBNNH4;
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ID OB
AC OB
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PRT;

PRELIMINARY;

287 361 347 409

74 99

Gaps

71;

Length 446;

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342 SPA---IQGEFEVPEELTLPCTMYDALRRLKGSALARELFGSEFVEGYVATKSMELTSFF 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 -----NTPRAFAICDAQELDGTPSGLSTRGLLKQVVARYAAHGLQPVVATELEFFVFA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 MSLQDAETEKNAFYDQNDEYGMSTLARNWIAGLLKYVPEATYFFASYINSYKRLQPLTFA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=16M / ATCC 21456 / Biotype 1;
MEDLINE=210020109; PubMed=11756688;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 ----NETYKSASQKHWKNLKTAQPHHQWMNISASSGIETFMRSVRNKLEEAGILMEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 HEMGTSQPEINFLHGDPVLLADQTFLFKHLLKEVALKHGLIVVCMAKPLAKTPGSSMHIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 QSIVELDGGRNIFSEADGE--PSAAFRHFIGGQACLADFTPFFAPHVNSFQRLCHPYAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 EGAVLAISNPHNFVTSE-----PLFCSPRVILMQQIERLANLKLKGLFASELEFNLF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 PNTDPNEPFQAPLGPDGRR----ELGYSAFSVSSNNGLRPFFEDVYRCMDALGLVRDTFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 PEFLPSOHELNFVPADPLTMADRHIIAKHGVREMAEQSGMVATFMAKLSSTALGNACHIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPASGNVYNDKELPE---PPNSLQNATHLLKESKMLNKTFGEKLILHYVNAANVEINEFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 LIGRHFLGLDQKKISISTFVYAVTIEGIAGGGYEISSVDTGYSDCHLCADLNSLHLLPWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTKCCWAIDNRTSAFRLCNSKSEGINVELRIGGADLNPYLAFSAIIAAGISGIEEKLELP
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                            + GLUTAMINE
                                                                                                                                                                                                                                                                                                                                                                                                          38;
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Brucellaceae; Brucella.
                                                                              ORTHOPHOSPHATE.

-!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.

EMBL; AE004758; AAG06744.1; --
HSSP; P60501; 1LGR.
INTERPRO; IPRO01637; GlnA adenyltn.
InterPro; IPR001691; GLN_Synth.
InterPro; IPR002155; Serpin.
  PA01,
                                                                                                                                                                                                                                                                                                                                                                                                          92; Mismatches 174; Indels
                                                              ADP
                                                                                                                                                                                                                            Pfan: PF00120; gln-synt; 1.
ProDom; PF001057; Gln-adenyltn; 1.
PROSITE; PS00284; SERPIN; 1.
Hypothetical protein; Ligase; Complete proteome.
SEQUENCE 413 AA; 45161 MW; 6989A0BF4122C375 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                            -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3)
                                                                                                                                                                                                                                                                                                                                                                  Score 469; DB 16;
Pred. No. 1.9e-30;
  of Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                  19.7%;
28.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                             Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                        Nature 406:959-964 (2000)
                    opportunistic pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KQVTDWE 446
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                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=29459;
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                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DTGYSDCHLCADLNSLHLLPWS-EGAVLAISNPHNFVT---SEPLFCSPRVILMQQIERL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304 YFFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCN---SKSEGINVELRIGGADLNP 360
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                                                                                                                                                                                                                                                                                                                                                                    GKIDTVVLACVDMQGRLMGKRLTGRHFLGLDQKKISISTFVYAVTIEGIAGGGY-EISSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 MRSVRNKLEEAGILMEATHPEFLPSOHELNFVPADPLTMADRHIIAKHGVREMAEOSGMV
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STRAINEATCC 15692 / PAO1;

MEDLINE=20437337; PubMed=10984043;

MEDLINE=20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Brwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino B., Westbrock Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K., Kas A., Larbig K., Lin R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                            STRAIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
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Tkeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005221; BAC18937.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa.
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
                                                                                                                                                                                                                                                                           Query Match
19.8%; Score 470.5; DB 16; Length 516;
Best Local Similarity 29.2%; Pred. No. 2e-30;
Matches 134; Conservative 85; Mismatches 167; Indels 73;
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SEQUENCE 516 AA; 58460 MW; 398C2255E226DC28 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein PA3356.
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NCBI_TaxID=152794;
                                            FROM N.A.
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Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Hagius S., O'Callaghan D., Letesson J.-J., Hagelkorn R., Kyrpides N., Overbeek R.; The genome sequence of the facultative intracellular pathogen Broc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).

REMBL, AEOGOS689, AAL53765.1; -. REMBL, AEOGOS689, AAL53765.1; -. REMBL, AEOGOS689, AAL53765.1; -. REMBL, PRO01620; Gln-Synth. Remai. PRO0120; Gln-Synth. Remai. PRO351; Gln-Synth. Remai. PRO351; Gln-Synth. 1. Remai. PRO351; Gln-Synth. 1. Remai. PRO351; Gln-Synth. 1. Remai. PRO351; Gln-Synth. 2. Remai. PRO351; Gln-Synth. 2. Remai. PRO351; Gln-Synth. 3. Remai. Brosont. 3. Remai. 3. Rem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 -----QWMNISASSGIETFMRSVRNKLEEAGILMEATHPEFLPSQHELNFVPADPLTM 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 GRAIGGGQGYSIAGVNEFDELIDDIYHFSEGQGLEIDTLIHEEGAGQLEINLRHGDPVEL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 ADRHIIAKHGVREMAEQSGMVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQNDEY 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 IRNGKIDTVVLA-----CV--DMOGRLMGKRLTGRHFLGLDQKKISISTFVYAVTIE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 GI---AGGGYEISSVDTGYSDCHLCADLNSLHLLPWSEGAVLAISNPHNFVTSEPLFCSP
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19.6%; Score 465; DB 16; Length 4'
Best Local Similarity 28.7%; Pred. No. 5.2e-30;
Matches 133; Conservative 71; Mismatches 208; Indels
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Search completed: December 17, 2003, 22:44:19 Job time : 45 secs

